Valproic acid reversed pathologic endothelial cell gene expression profile associated with ischemia–reperfusion injury in a swine hemorrhagic shock model

Marlin Wayne Causey, MD,[a] Shashikumar Salgar, PhD,[b] Niten Singh, MD,[a] Matthew Martin, MD,[a] and **Jonathan D. Stallings, PhD,[b]** *Tacoma, Wash*

Background: **Vascular endothelial cells serve as the first line of defense for end organs after ischemia and reperfusion injuries. The full etiology of this dysfunction is poorly understood, and valproic acid (VPA) has proven to be beneficial after traumatic injury. The purpose of this study was to determine the mechanism of action through which VPA exerts its beneficial effects.**

Methods: **Sixteen Yorkshire swine underwent a standardized protocol for an ischemia–reperfusion injury through hemorrhage and a supraceliac cross-clamp with ensuing 6-hour resuscitation. The experimental swine (n = 6) received VPA at cross-clamp application and were compared with sham (n = 5) and injury-control models (n = 5). Aortic endothelium was harvested, and microarray analysis was performed along with a functional clustering analysis with gene transcript validation using relative quantitative polymerase chain reaction.**

Results: **Clinical comparison of experimental swine matched for sex, weight, and length demonstrated that VPA significantly decreased resuscitative requirements, with improved hemodynamics and physiologic laboratory measurements. Six transcript profiles from the VPA treatment were compared with the 1536 gene transcripts (529 up and 1007 down) from sham and injury-control swine. Microarray analysis and a Database for Annotation, Visualization and Integrated Discovery functional pathway analysis approach identified biologic processes associated with pathologic vascular endothelial function, specifically through functional cluster pathways involving apoptosis/cell death and angiogenesis/vascular development, with five specific genes (*THBS1*, *TNFRSF12A*, *ANGPTL4*, *RHOB*, and *RTN4*) identified as members of both functional clusters. This study also examined gene expression of transforming growth factor (TGF)-β (TGF-β1, TGF-β2, and TGF-β-releasing thrombospondin 1 [THBS1]) and genes expressing vascular endothelial growth factor (VEGF) C, VEGFD, and VEGFR1 and found that these genes were involved in the endothelial functional preservation associated with VPA administration.**

Conclusions: **VPA minimized pathologic endothelial cell function through the TGF-β and VEGF functional pathways. This study also implicates that integrated functional modeling and analysis will enable advancements in endothelial dysfunction using a systems biology approach. (J Vasc Surg 2012;55:1096-103.)**

Clinical Relevance: **The functional pathways associated with vascular ischemia–reperfusion are not fully understood. This study found that valproic acid (VPA), administered along with the application of a supraceliac cross-clamp, improved clinical, physiologic, and histologic changes in a swine model of hemorrhage and ischemia–reperfusion: 35% blood volume hemorrhage, 50-minute supraceliac aortic cross-clamp, and a 6-hour resuscitation. A functional analysis of endothelial dysfunction, with relative quantitative polymerase chain reaction validation, demonstrated the initial changes in endothelial cell dysfunction occurred through vascular endothelial growth factor and transforming growth factor-β gene members. This study demonstrates that pharmaceutical agents administered with an ischemic injury are beneficial after ischemia and target two common functional endothelial pathways.**

The molecular pathways altered with vascular ischemia are not fully understood. Previously, basic science research into endothelial and vascular ischemia–reperfusion injury centered on free radical scavenging and minimizing injury once it had occurred.[1-3] During the past 2 decades, however, there has been a transition in researching free radical scavenging to an analysis of pharmacologic agents that would minimize autogenous injury through a reduction in

From the Departments of Surgery[a] and Clinical Investigation,[b] Madigan Healthcare System, Joint Base Lewis-McChord.

The views expressed are those of the author(s) and do not reflect the official policy of the Department of the Army, the Department of Defense, or the U.S. Government. The investigators adhered to the policies for protection of human subjects as prescribed in Title 45 of the Code of Federal Regulations, Part 46.

This manuscript was the Norman Rich Award recipient for the 2010 Military Vascular Surgery Society and was presented at the podium at the 2011 Peripheral Vascular Surgery Society meeting, Chicago, Ill, Jun 15, 2011.

Competition of interest: none.

Additional material for this article may be found online at www.jvascsurg.org.

Reprint requests: Marlin Wayne Causey, 9040 Jackson Ave, Tacoma, WA 98431 (e-mail: mwcausey@msn.com).

The editors and reviewers of this article have no relevant financial relationships to disclose per the JVS policy that requires reviewers to decline review of any manuscript for which they may have a competition of interest.

0741-5214/$36.00

Published by Elsevier Inc. on behalf of the Society for Vascular Surgery.

doi:10.1016/j.jvs.2011.08.060

cellular metabolic demand before an ischemic insult. This is important, because maintenance of physiologic homeostasis after major resuscitative efforts is crucial, and most current studies have focused on the effect of intravenous crystalloids and use of vasopressors because these are widely used to augment adequate tissue perfusion by maintaining homeostatic cardiovascular and hemodynamic parameters.[4,5]

The vascular endothelial cell layer is now widely recognized as a critical component in maintaining physiologic homeostasis and regulating normal as well as pathologic responses to injury. Disruption or injury of the vascular endothelial cell layer initiates a broad cascade of local and systemic processes that involve the coagulation system, the inflammatory cascade, and the cellular immune system. This has been implicated in adverse outcomes among a wide variety of patient populations, including acute and chronic vasculopathy, vascular and endovascular surgery, and after major traumatic injury. It is likely that the pathogenesis of temporary ischemia involves oxidative damage and metabolic disturbances that ultimately lead to dysregulation of endothelial gene expression.[6] Because vascular homeostasis is linked with the acquisition of aberrations in the gene-regulatory programs,[7,8] our group has used a microarray approach to examine gene expression changes in injured aortic endothelial cells after hemorrhagic shock as part of a model validation.[6]

Our porcine surgical model of hemorrhagic shock and functional clustering analysis demonstrated significant changes in members of the transforming growth factor-β (TGF-β) and vascular endothelial growth factor (VEGF) gene families in the endothelium, suggesting that angiogenesis, vascular permeability, and apoptotic pathways are critical to endothelial cellular dysfunction as the result of hemorrhagic shock. Major mechanisms involved in the alteration and regulation of gene expression include local chromatin remodeling and alterations in nucleosomal packaging of DNA, primarily through covalent posttranslational modifications of nucleosomal histones by acetylation, methylation, phosphorylation, and ubiquitination.[9]

In addition to the previously identified TGF-β and VEGF pathways, gene-regulatory states are established and maintained by chromatin-modifying enzymes,[10] such as histone acetyltransferases and histone deacetylases (HDACs), making these enzymatic pathways attractive and obvious targets for pharmacologic therapy. One readily available and widely used agent is valproic acid (VPA, 2-propylpentanoic acid), an HDAC inhibitor.[11,12] Drugs that target histone acetyltransferases and HDAC activities may provide cytoprotective effects, resulting in less demand for aggressive resuscitative efforts, and could significantly improve outcome after hemorrhage.[12] Although established as a long-term treatment for epilepsy, bipolar disorders, migraine, and neuropathic pain, several in vitro models have demonstrated that VPA attenuates expression of angiogenic and vascular permeability factors.[13] Many possible pathways exist in the etiologic benefit of VPA[13]; however, it is likely that these actions are the result of HDAC inhibitor activity, causing histone hyperacetylation.[14] Indeed, VPA activates cell survival factors[15] and offers significant HDAC inhibition-mediated neuroprotection in models of cerebral ischemia.[16]

VPA may mitigate changes in vascular gene expression patterns and preserve overall vascular endothelial function, because several in vitro models have demonstrated that VPA attenuates expression of both angiogenic and vascular permeability factors.[6] The in vivo profile of VPA in humans is well characterized. The drug is easily administered and shows good pharmacokinetics, with a clinically useful half-life of 15.9 to 17.3 hours.[17]

We initiated this follow-on study to determine whether VPA altered endothelial pathway members, such as TGF-β and VEGF, in vivo and to determine the clinical, physiologic, and hemodynamic benefit in our porcine model of hemorrhagic shock with transient ischemia and subsequent reperfusion. Here, we report changes in endothelial gene expression and the identification of altered functional clusters as the result of treatment with VPA in six swine that received this injury compared with the model validation protocol that our group previously published.[6]

METHODS

This study was approved by the Madigan Army Medical Center Institutional Animal Care and Use Committee.

Hemorrhagic shock and ischemia-reperfusion injury model. Sixteen Yorkshire swine were purchased from a U.S. Department of Agriculture–approved swine research facility and housed in accordance with the *Guidelines for the Care and Use of Laboratory Animals.*[18]

Animals were anesthetized, intubated, and vascular access was obtained to continuously monitor central and peripheral cardiovascular hemodynamics. A midline celiotomy permitted placement of catheters in the bladder and inferior vena cava and enabled application of a supraceliac aortic cross-clamp. Hemorrhage (35% of total circulating blood volume) was induced through the inferior vena cava catheter over 30 minutes, followed by 50 minutes of ischemia through the supraceliac aortic cross-clamp, followed by reperfusion and a 6-hour resuscitative phase.[6]

The protocol called for strict measures to maintain the mean arterial blood pressure (>40 mm Hg), temperature, and ventilator parameters. Continuous arterial, pulmonary, and central venous pressures were also recorded. Blood samples were collected for laboratory analysis every 15 minutes before and during the cross-clamp setup and application and every 30 minutes during the 6-hour resuscitation (Fig 1).

Isolation of endothelial RNA and porcine genome microarray. Immediately after euthanasia, the aorta below the cross-clamp area was harvested and washed using sterile ice-cold phosphate buffered saline. The aortic wall was cut longitudinally and mounted on a platform to expose the endothelial surface. The endothelial surface (~1-in^2) was covered with 200-μL lysis buffer (High Pure RNA isolation kit, Roche Diagnostics, Mannheim, Germany) and gently scraped with a sterile scalpel. The scraped endothelial cells

Fig 1. Study protocol depicts the timeline of interventions. Of note, the cross-clamp was placed on the supraceliac aorta. *IJ,* Internal jugular; *IVC,* inferior vena cava; *PA,* pulmonary artery; *VPA,* valproic acid.

with buffer were aspirated and transferred to an RNAse-free sterile vial and the process was repeated two to three times.

Total RNA was amplified using a MessageAmp III RNA Amplification kit (Ambion, Austin, Tex), and the amplified complimentary RNA was biotinylated, fragmented, and probe hybridized to an Affymetrix GeneChip (Affymetrix, Santa Clara, Calif). Affymetrix GeneChip Porcine Genome hybridization raw pixel analysis was performed at a commercial facility (Benaroya Institute, Seattle, Wash). Raw pixel files were analyzed using Affymetrix Gene Chip Operating Software (GCOS 1.4), as previously described.[6]

Gene expression (messenger RNA transcript level) was measured in the total RNA that was used for genomic microarray analysis by relative quantitative polymerase chain reaction (qPCR) using a 96-well LightCycler 480 platform (Roche Applied Science, Mannheim, Germany) and one-shot method Light Cycler 480 RNA Master Hydrolysis Kit. Briefly, primers for all selected genes were constructed, and specific probes were chosen by using Roche's Universal Probe Library Assay Design Center software. PCR was performed using 50 to 100 ng of total RNA template, 0.5 μmol/L primers, and 0.25 μmol/L hydrolysis probe according to the manufacturer's recommendations (Roche Applied Science, Indianapolis, Ind).

Each sample was run in triplicates for the target gene and for phosphoglycerate kinase 1 (PGK1; an internal control), a housekeeping gene that was expressed at relatively consistent levels in all samples. The target gene transcripts were normalized to PGK1 (target gene: *PGK1*) with target genes *TGF-β1, TGF-β2,* TGF-β-releasing thrombospondin 1 (*THBS1*), *VEGFR1, VEGFC,* and *VEGFD*. To easily compare results from microarray and relative qPCR, both data are presented as relative fold-change compared with sham controls.

Statistical analysis. Physiologic and laboratory parameters, with a primary end point measure being resuscitative requirements and secondary end points being acidosis (pH and lactate), coagulopathy (international normalized ratio), cardiac index, and systemic vascular resistance index, were compared using a *t* test to analyze the differences in the final measurements collected at resuscitation hour 6 using PASW 18.0 software (PASW, Chicago, Ill).

Through a comparison with our previously published data,[6] distribution of raw microarray data, coefficient of variance, determination of thresholds, and additional *t* tests were performed using Excel 2007 software (Microsoft Corp, Redmond, Wash) to include single and batch GeneChip analysis performed in GCOS of 1536 genes previously identified. Gene detection (present, marginal, or absent) was based on a computed discrimination score of 0.8 (the ratio for each probe pair) and a τ value of 0.015, The gene detection *P* value was determined by a one-sided Wilcoxon signed-rank test, which was also used in the comparison analysis to determine biologic statistical significance. Each probe set signal was compared with the baseline array signal and a change in *P* value was determined by GCOS. Lists, including the upregulated and downregulated pig gene, were annotated[19] to their corresponding human counterparts using Database for Annotation, Visualization and Integrated Discovery (DAVID) Bioinformatics Resources 6.7 (National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Md) as previously described.[20,21]

RESULTS

Clinical comparison with experimental swine matched for sex, weight, and length demonstrated that VPA significantly decreased resuscitative requirements and improved overall hemodynamics and physiologic laboratory measurements. There was a significant decrease in resuscitative requirements as measured by isotonic crystalloids infusion ($P < .05$), the total epinephrine dose required during resuscitation ($P < .01$), and improvements in hemodynamics and standard physiologic laboratory measures (Table I). Given the significant findings of overall improved physiologic measures, microarray analysis with DAVID functional cluster analysis was performed. Six transcript profiles from the VPA treatment were compared with the 1536 gene transcripts (529 up and 1007 down; see the Appendix [online only] for the raw pixel values and the ratio of sham/VPA and injury/VPA) from the model validation

Table I. Physiologic parameters[a]

Physiologic variable	*Sham Mean (SEM)*	*Injury Mean (SEM)*	*VPA Mean (SEM)*
Total resuscitative requirements			
Epinephrine, grams	—	14.5 (3.05)	4.89 (0.68)[b]
Crystalloid fluids, liters	3.89 (0.80)	20.14 (2.38)	13.33 (1.29)[c]
Hemodynamic (after cross-clamp release)			
pH	7.47 (0.007)	7.04 (0.011)	7.21 (0.008)[d]
Lactate, mmol/L	2.45 (0.13)	11.97 (0.18)	12.62 (0.21)
Bicarbonate, mEq/L	33.73 (0.47)	12.93 (0.35)	16.85 (0.27)[d]
Fibrinogen, mg/dL	179.00 (3.55)	85.82 (2.93)	102.88 (3.20)[c]
Hematocrit, % RBC	25.56 (0.52)	15.84 (0.60)	15.77 (0.35)
International normalized ratio	0.87 (0.01)	1.67 (0.10)	1.21 (0.04)[d]
Cardiac output, L/min	3.65 (0.17)	5.53 (0.40)	5.89 (0.21)
SVR, dyn · s · cm^{-5}	1193.61 (62.22)	893.38 (52.03)	531.40 (39.18)[d]

RBC, Red blood cells; *SEM,* standard error of the mean; *SVR,* systemic vascular resistance; *VPA*, valproic acid.
[a]Analysis of variance multivariate analysis was used to examine total resuscitative requirements. General linear model of repeated measures was used to examine physiologic parameters throughout the resuscitative efforts (values represent the estimated marginal means from time points 1.5 through 6 hours after cross-clamp release). Bonferroni post hoc analysis was used to determine significance between injury and VPA pigs: [b]$P < .1$; [c]$P < .01$; [d]$P < .001$.

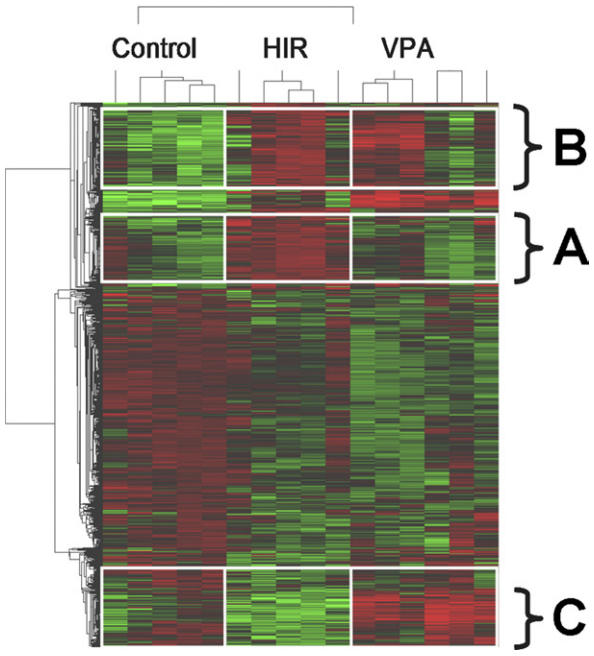

Fig 2. Heat map (*red,* higher expression; *green,* lower expression) demonstrated significant changes in gene expression in three areas. Identified were **(A)** 183 genes that valproic acid (*VPA*) treatment reversed, similar to sham pigs; (**B**) 232 genes that were similar to sham in only 50% of the VPA-treated pigs; and **(C)** genes that were unlike the sham or VPA-treated or untreated hemorrhage injury-control (*HIC*) swine.

experiments[6] using cluster 3.0, and the data were organized into a gene dendrogram using TreeView.

As shown in Fig 2, the heat map (red, higher expression; and green, lower expression) demonstrated significant changes in gene expression in three areas: First, 183 genes were identified that VPA treatment reversed (Fig 2, *A*), similar to sham pigs. Second, we identified a group of 232 genes that were similar to sham in only 50% of the VPA-treated pigs (Fig 2, *B*). Third, there was a group of genes that were unlike the sham or the VPA-treated or untreated injury control swine (Fig 2, *C*).

A DAVID functional analysis was performed by using the porcine genome and the corresponding annotated human Ensembl ID[19] to identify the functional manner in which these genes interact. Of the 574 genes analyzed, 502 were identified and eight were unknown. On medium classification stringency (DAVID default setting), 196 annotation clusters were identified, of which 12 demonstrated an enrichment score of >2. Of the 196 clusters, four were biologic processes related to ribosome metabolism, apoptosis and cell death, angiogenesis and vascular development, and cell migration and locomotion (Table II). All of the members for each gene ontology (GO) term within cluster 5 and 6 (ie, GO:000821–cell death and GO: 0042981–regulation of apoptosis, which have 40 and 42 members identified, respectively) were combined and unique members identified (Table III and Table IV, respectively). Cluster 5 (apoptosis and cell death) contained 59 unique members, and cluster 6 (angiogenesis and vascular development) contained 18 unique members. Five genes (*THBS1, TNFRSF12A, ANGPTL4, RHOB*, and *RTN4*) were identified as members of both functional clusters.

To validate our microarray findings, we analyzed the gene expression of TGF-β (TGF-β1, TGF-β2, and THBS1) and VEGF (VEGFR1, VEGFC, and VEGFD) members. To allow for easy comparison, relative qPCR values and microarray values were represented as fold-change (Fig 3, *A-F*). TGF-β1 and TGF-β2 expression coincided with the microarray results (Fig 3, *A and B*), but THBS1 did not (Fig 3. *C*). The most striking results were evident with VEGF members, in which VEGFR1, VEGFC, and VEGFD coincided with our microarray results (Fig 3, *D-F*). VPA reversed the pathologically induced overexpres-

Table II. Database for Annotation, Visualization and Integrated Discovery functional gene cluster analysis: Biologic processes associated with valproic acid-treated ischemia–reperfusion injury in a hemorrhagic shock model

Term	*Count (%)*	P	*Benjamini*
Cluster 1: Enrichment score: 5.13			
GO:0042254–ribosome biogenesis	19 (3.785)	1.28^{-8}	<.001
GO:0022613–ribonucleoprotein complex biogenesis	21 (4.183)	2.58^{-7}	<.001
GO:0034660–noncoding RNA metabolic process	23 (4.582)	8.91^{-7}	<.001
GO:0006364–ribosomal RNA processing	14 (2.789)	2.27^{-6}	<.001
GO:0016072–ribosomal RNA metabolic process	14 (2.789)	3.70^{-6}	<.001
Cluster 5: Enrichment score: 3.04			
GO:0008219–cell death	40 (7.968)	1.13^{-4}	<.05
GO:0016265–death	40 (7.968)	1.31^{-4}	<.05
GO:0042981–regulation of apoptosis	42 (8.367)	2.83^{-4}	<.05
GO:0043067–regulation of programmed cell death	42 (8.367)	3.47^{-4}	<.05
GO:0010941–regulation of cell death	42 (8.367)	3.78^{-4}	<.05
Cluster 6: Enrichment score: 3.01			
GO:0001525–angiogenesis	14 (2.789)	3.61^{-4}	<.05
GO:0048514–blood vessel morphogenesis	17 (3.386)	4.24^{-4}	<.05
GO:0001568–blood vessel development	18 (3.586)	7.82^{-4}	<.1
GO:0001944–vasculature development	18 (3.586)	.001021	<.1
Cluster 7: Enrichment score: 2.79			
GO:0030334–regulation of cell migration	15 (2.988)	3.96^{-4}	<.1
GO:0040012–regulation of locomotion	16 (3.187)	4.65^{-4}	<.1

GO, Gene ontology.

sion of each VEGF member, particularly VEGFC, which was reduced by 13-fold compared with the injured group. This was the third-highest VPA-induced change in gene expression observed among the 1536 genes analyzed.

DISCUSSION

Relative or complete vascular ischemic injury occurs in many clinical scenarios of interest to the trauma and vascular surgery community. Occlusive control of arterial blood flow is often needed in trauma, elective surgical procedures, and endovascular interventions. Even in the absence of surgical vascular occlusion, the impaired or inadequate perfusion seen in severe hemorrhagic shock and other disease states can produce a significant global or local ischemic burden. A host of endogenous compensatory mechanisms are stimulated, such as vasoconstriction and the shunting of blood, which help to mitigate injury to vital organs and the brain. After an ischemic insult, these endogenous mechanisms are insufficient for full compensation and, combined with the reperfusion of toxic metabolic by-products, lead to significant endothelial dysfunction that ultimately contributes to the loss of intrinsic physiologic homeostasis, which may be manifested as systemic inflammation and end-organ failure after reperfusion.

Indeed, recent advances in the Human Genome Project and molecular medicine have prompted a number of laboratories to investigate pharmacologically based approaches to reduce the physiologic demand of host tissues. The overarching hypothesis is that reducing host tissue demands in concert with appropriate (ie, decreased requirements for) fluid and vasopressor resuscitation may ultimately lead to greater survival and a decreased incidence of pathologic sequela associated with periods of ischemia and reperfusion. One such pharmacologic agent is VPA, which is known to inhibit expression of apoptosis- and angiogenic-related factors in vitro,[22] with similar biologically relevant pathways altered by VPA treatment that were identified in vivo by microarray and functional clustering analysis in the current study. Our results indicate that VPA not only improves physiologic parameters but also reverses some of the transcriptional changes that occur in endothelial cells of swine that receive a hemorrhage shock injury. Whether alteration of these functional pathways in endothelial cells directly improved outcome has yet to be tested and is the focus of our future work.

The mainstay of therapy for treatment of patients in shock states has been aimed at therapies to increase and improve fluid and oxygen delivery to end-organ tissues. This includes minimizing any periods of vascular occlusion, restoring the flow of oxygenated blood, and administering resuscitative fluids such as crystalloids, colloids, and blood products. All of these therapies are aimed at restoring adequate (or even supranormal) macroperfusion and microperfusion and can be thought of as "supply-side" treatment. However, there are also well-described limitations and adverse effects of this approach, including pathologic immune modulation, fluid overload, and compartment syndromes, as well as failure of resuscitation caused by delayed initiation or overwhelming ischemic injury.

An alternative (and likely complementary) approach would focus on the "demand side" of the shock equation and target interventions that would induce metabolic protection or cellular tolerance to ischemia–reperfusion. The rationale behind VPA administration is to alter the demand-side physiology and mitigate injury by targeting the vascular endothelium, which serves as the barrier between toxic metabolic by-products and critical end organs. Through a decrease in the metabolic demand and induced tolerance of

Table III. Cluster 5 gene list and corresponding gene ontology (*GO*) terms (apoptosis and cell death pathways), 59 members altered by valproic acid treatment

	GO term				
Gene symbol	*0008219*	*0016265*	*0042981*	*0043067*	*0010941*
CABC1	X	X			
TMEM123	X	X			
SLC33A1	X	X			
OLR1	X	X			
GARS	X	X			
CJA1	X	X			
PDE1B	X	X			
YARS	X	X			
MAGI1	X	X			
NEK11	X	X			
PTRH2	X	X			
TNFRSF12A[a]	X	X			
CASP7	X	X			
RHOB[a]	X	X			
TCTN3	X	X			
C8ORF4	X	X			
DIO1	X	X			
PKCA			X	X	X
TUBBP2			X	X	X
FOSL1			X	X	X
PTPRF			X	X	X
PTGS1			X	X	X
NACC1			X	X	X
INHBA			X	X	X
EIF5A			X	X	X
EEF1E1			X	X	X
SORT1			X	X	X
ASNS			X	X	X
NME1			X	X	X
ANGPTL4[a]			X	X	X
MITF			X	X	X
PDE3A			X	X	X
HSPA9			X	X	X
AMIGO2			X	X	X
CCL2			X	X	X
YWHAZ			X	X	X
TGFB1	X	X	X	X	X
RTN4[a]	X	X	X	X	X
MSFL	X	X	X	X	X
TIAM2	X	X	X	X	X
BID	X	X	X	X	X
PSME3	X	X	X	X	X
TNFRSF16	X	X	X	X	X
CAM-1	X	X	X	X	X
PHLDA1	X	X	X	X	X
CYCS	X	X	X	X	X
TRIM35	X	X	X	X	X
POLB	X	X	X	X	X
KRAS	X	X	X	X	X
GRIK2	X	X	X	X	X
AATF	X	X	X	X	X
THBS1[a]	X	X	X	X	X
MYCL1	X	X	X	X	X
SOD2	X	X	X	X	X
IER3	X	X	X	X	X
SMS1	X	X	X	X	X
BAG1	X	X	X	X	X
BIRC6	X	X	X	X	X
BNIP3L	X	X	X	X	X

[a]These genes are also members of cluster 6.

Table IV. Cluster 6 gene list and corresponding gene ontology (*GO*) terms (angiogenesis and vascular development pathways), 18 members altered by valproic acid treatment

	GO term			
Gene symbol	*0001525*	*0048514*	*0001568*	*0001944*
ITGAV			X	X
MYO1E		X	X	X
GJC1		X	X	X
ZMIZ1		X	X	X
CXCL12	X	X	X	X
PTK2	X	X	X	X
RTN4[a]	X	X	X	X
NCL	X	X	X	X
IL-18	X	X	X	X
THBS1[a]	X	X	X	X
CYR61	X	X	X	X
ANGPTL4[a]	X	X	X	X
VEGFC	X	X	X	X
NARG1	X	X	X	X
TNFRSF12A[a]	X	X	X	X
FLT1 (or *VEGFR1*)	X	X	X	X
RHOB[a]	X	X	X	X
FIGF (or *VEGFD*)	X	X	X	X

[a]These genes are also members of cluster 5.

ischemia–reperfusion injury, we suspect that pharmaceutical agents aimed at minimizing cellular demand physiology will allow cellular survival that has not been previously possible with fluid resuscitation alone. Currently, there has been much focus on VPA because this agent has shown promise in cellular protection after periods of ischemia or hemorrhage, but these pathways are largely unknown.[23-25]

Our results have identified factors related to apoptosis/cell death and angiogenesis/vascular development as being among the major pharmacologic targets of VPA after a severe ischemia–reperfusion injury, particularly VEGF and TGF-β. Although it is possible that changes in hemodynamic factors and other aspects of the injury contributed to the changes in gene expression in the VPA-treated animals, the genes we discovered that changed have been identified as transcriptional targets of VPA in several in vitro models. Thus, our results are the first to support these gene families as targets of VPA action in vivo. Whereas TGF-β is well known to be involved in cell survival and apoptosis, VEGF members are known to play a critical role in regulating major angiogenic and lymphoangiogenic factors that regulate multiple endothelial cell functional pathways. Angiogenesis itself is a very complex, tightly regulated, multistep process, and the targeting of this pathway may prove useful in advancing the clinical use of novel therapeutic agents.

Microarray analysis is a useful tool in determining gene expression, but understanding the true effect of the results is tricky and even misleading. We sought to minimize these limitations by first validating our model and ensuring that gene expression variability was minimized through the analysis of data obtained from multiple swine in each

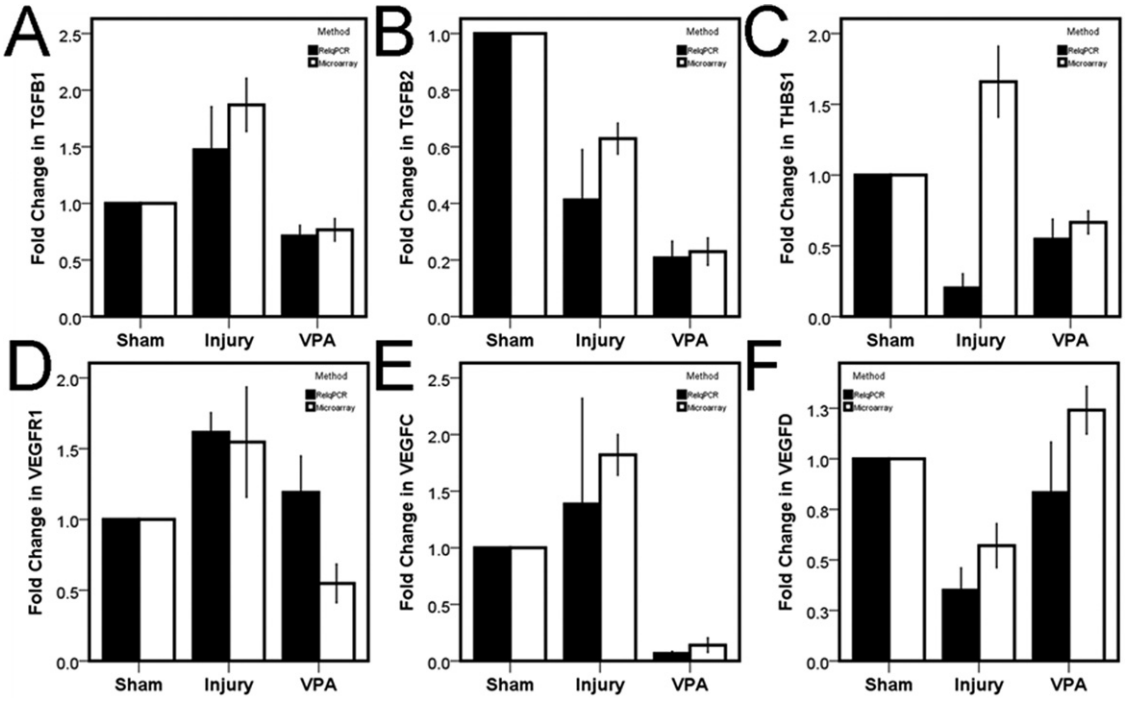

Fig 3. Comparison shows relative quantitative polymerase chain reaction results (*black bars*) with microarray results (*open bars*). Data are represented as fold-change with the standard deviation (*error bars*). **A**-**D**, Analysis is shown for the mean relative transcript (*black bars*) from four sham, three injured, and five valproic acid (*VPA*) specimens in triplicate from sham, injury, and VPA animals vs five sham, five injured, and six VPA microarray results. **E** and **F**, The same analysis is represented; however, enough RNA remained to run an analysis of two injured animals.

group. To further minimize the potential limitations in the interpretation of gene expression data, we performed a functional analysis by identifying those genes that were functionally related and comparing with previous data supporting their interactions (DAVID analysis). We used relative qPCR to validate the relative changes in gene expression observed by our microarray analysis with a direct comparison to the microarray analysis results.

It is in this area of microarray research that a systems biology approach is needed to fully integrate the transcriptomic, epigenomic, proteomic, and metabolomic alterations of ischemia–reperfusion into a predictable and clinically useful biologic model of injury. A complete temporal and spatial analysis of the system pathways involved in endothelial injury is necessary to better understand the full effect on systemic injury and to better predict how to use resuscitative and pharmacologic approaches to treat patients as early as possible. Full integration of these systems across time and space throughout the vasculature, analysis of physiologic parameters, and course of treatments will allow a full analysis of the overall physiologic response to injury and an experimental intervention and needs to be analyzed within each organ system independently. This process is essential when analyzing pharmacologic interventions to predict the severity of injury, tolerance and effect of treatments, and potentially construct an individualized approach from real-time data to fully maximize patients who would best benefit from treatment of an ischemic injury.

CONCLUSIONS

VPA administration demonstrated a significant benefit when used as an adjunct to resuscitation in a swine model of hemorrhage coupled with ischemia–reperfusion injury. This included a drastic decrease in crystalloid and epinephrine requirements as well as improvements in physiologic and hemodynamic parameters. Microarray analysis and a DAVID functional analysis identified four biologic processes that were altered in the vascular endothelium as early as 6 hours after ischemia, specifically involving apoptosis/cell death and angiogenesis/vascular development, with five specific genes (*THBS1, TNFRSF12A, ANGPTL4, RHOB,* and *RTN4*) identified as members of both functional clusters. This study also examined gene expression of TGF-β (TGF-β1, TGF-β2, and THBS1) and VEGF (VEGFC, VEGFD, and VEGFR1) members, many of which are known mediators of endothelial dysfunction, to validate our microarray results. The findings of this study demonstrate the positive effect of VPA administration on preserving large-vessel endothelial function in a model of severe traumatic shock. Further studies are warranted to investigate the clinical applicability and underlying mechanisms of this promising pharmacologic adjunct.

We thank Laurie Huston for her isolation of endothelial cells and preparation of the samples for microarray analysis and Mary DeHart for her technical assistance with relative qPCR.

AUTHOR CONTRIBUTIONS

Conception and design: MC, MM, JS
Analysis and interpretation: MC, SS, JS
Data collection: MC, SS, JS
Writing the article: MC, SS, NS, MM, JS
Critical revision of the article: MC, NS, MM, JS
Final approval of the article: MC, NS, MM, JS
Statistical analysis: MC, SS, JS
Obtained funding: MC, MM, JS
Overall responsibility: MC

REFERENCES

1. Bourchier RG, Gloviczki P, Larson MV, Wu QH, Hallett JW Jr, Ahlquist DA, et al. The mechanisms and prevention of intravascular fluid loss after occlusion of the supraceliac aorta in dogs. J Vasc Surg 1991;13:637-45.
2. Ricci MA, Graham AM, Corbisiero R, Baffour R, Mohamed F, Symes JF. Are free radical scavengers beneficial in the treatment of compartment syndrome after acute arterial ischemia? J Vasc Surg 1989;9:244-50.
3. Ouriel K, Smedira NG, Ricotta JJ. Protection of the kidney after temporary ischemia: free radical scavengers. J Vasc Surg 1985;2:49-53.
4. Moore FA, McKinley BA, Moore EE, Nathens AB, West M, Shapiro MB, et al. Inflammation and the host response to injury, a large-scale collaborative project: patient-oriented research core–standard operating procedures for clinical care. III. Guidelines for shock resuscitation. J Trauma 2006;61:82-9.
5. Spahn DR, Cerny V, Coats TJ, Duranteau J, Fernández-Mondéjar E, Gordini G, et al. Management of bleeding following major trauma: a European guideline. Crit Care 2007;11:R17.
6. Causey MW, Hoffer ZS, Miller SL, Huston LJ, Satterly SA, Martin M, et al. Microarray and functional cluster analysis implicates transforming growth factor beta1 in endothelial cell dysfunction in a swine hemorrhagic shock model. J Surg Res 2011;170:120-32.
7. Alam HB, Stegalkina S, Rhee P, Koustova E. cDNA array analysis of gene expression following hemorrhagic shock and resuscitation in rats. Resuscitation 2002;54:195-206.
8. Zamora R, Vodovotz Y, Aulak KS, Kim PK, Kane JM 3rd, Alarcon L, et al. A DNA microarray study of nitric oxide-induced genes in mouse hepatocytes: implications for hepatic heme oxygenase-1 expression in ischemia/reperfusion. Nitric Oxide 2002;7:165-86.
9. Khochbin S, Wolffe AP. The origin and utility of histone deacetylases. FEBS Lett 1997;419:157-60.
10. Kouzarides T. Acetylation: a regulatory modification to rival phosphorylation? EMBO J 2000;19:1176-9.
11. Gonzales E, Chen H, Munuve R, Mehrani T, Britten-Webb J, Nadel A, et al. Valproic acid prevents hemorrhage-associated lethality and affects the acetylation pattern of cardiac histones. Shock 2006; 25:395-401.
12. Gonzales ER, Chen H, Munuve RM, Mehrani T, Nadel A, Koustova E. Hepatoprotection and lethality rescue by histone deacetylase inhibitor valproic acid in fatal hemorrhagic shock. J Trauma 2008;65:554-65.
13. Blaheta RA, Cinatl J Jr. Anti-tumor mechanisms of valproate: a novel role for an old drug. Med Res Rev 2002;22:492-511.
14. Phiel CJ, Zhang F, Huang EY, Guenther MG, Lazar MA, Klein PS. Histone deacetylase is a direct target of valproic acid, a potent anticonvulsant, mood stabilizer, and teratogen. J Biol Chem 2001; 276:36734-41.
15. De Sarno P, Li X, Jope RS. Regulation of Akt and glycogen synthase kinase-3 beta phosphorylation by sodium valproate and lithium. Neuropharmacology 2002;43:1158-64.
16. Ren M, Leng Y, Jeong M, Leeds PR, Chuang DM. Valproic acid reduces brain damage induced by transient focal cerebral ischemia in rats: potential roles of histone deacetylase inhibition and heat shock protein induction. J Neurochem 2004;89:1358-67.
17. Grover A, Benet LZ. Intermittent drug dosing intervals guided by the operational multiple dosing half lives for predictable plasma accumulation and fluctuation. J Pharmacokinet Pharmacodyn 2011; 38:369-83.
18. Institute of Laboratory Animal Research, Commission on Life Sciences, National Research Council. Guide for the care and use of laboratory animals. Washington, DC: National Academy Press; 1996.
19. Tsai S, Cassady JP, Freking BA, Nonneman DJ, Rohrer GA, Piedrahita JA. Annotation of the Affymetrix porcine genome microarray. Anim Genet 2006;37:423-4.
20. Dennis G Jr, Sherman BT, Hosack DA, Yang J, Gao W, Lane HC, et al. DAVID: Database for Annotation, Visualization, and Integrated Discovery. Genome Biol 2003;4:3.
21. Huang da W, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nat Protoc 2009;4:44-57.
22. Dong XF, Song Q, Li LZ, Zhao CL, Wang LQ. Histone deacetylase inhibitor valproic acid inhibits proliferation and induces apoptosis in km^3 cells via downregulating VEGF receptor. Neuro Endocrinol Lett 2007;28:775-80.
23. Alam HB, Shuja F, Butt MU, Duggan M, Li Y, Zacharias N, et al. Surviving blood loss without blood transfusion in a swine poly-trauma model. Surgery 2009;146:325-33.
24. Li Y, Liu B, Dillon ST, Fukudome EY, Kheirbek T, Sailhamer EA, et al. Identification of a novel potential biomarker in a model of hemorrhagic shock and valproic acid treatment. J Surg Res 2010;159:474-81.
25. Li Y, Liu B, Sailhamer EA, Yuan Z, Shults C, Velmahos GC, et al. Cell protective mechanism of valproic acid in lethal hemorrhagic shock. Surgery 2008;144:217-24.

Submitted Jun 14, 2011, accepted Aug 18, 2011.

Additional material for this article may be found online at www.jvascsurg.org.

Appendix (online only). Raw pixel values for data from the sham, control, and valproic acid (VPA) experimental groups for the 1536 gene transcripts

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.773.1.S1_at, BI403077, HIST1H2BK	452.4	488.4	309.4	1124.3	581.5	294.2	168.0	265.1	93.8	266.6
Ssc.8811.1.S1_at, BI181293	260.4	243.2	265.0	221.8	472.0	311.2	132.9	56.8	82.3	223.7
Ssc.21027.2.A1_a_at, CN166755, BNIP3L	201.6	200.5	146.9	173.2	278.4	143.2	102.1	122.3	82.3	172.7
Ssc.20017.1.A1_at, BQ600530, MYH10	1532.1	1112.7	1213.2	551.9	1348.3	1236.8	705.8	762.1	425.1	678.6
Ssc.25636.1.S1_at, BX920064	133.4	264.2	106.5	211.1	428.1	118.6	107.8	253.6	97.3	180.7
Ssc.8893.1.A1_at, BF708608, AMBRA1	592.1	270.5	345.4	95.7	187.7	667.9	318.6	484.1	1099.9	435.2
Ssc.24446.1.A1_at, CN032148, DDX21	740.8	416.7	417.7	132.9	178.3	567.9	616.0	621.0	1183.3	224.4
Ssc.12829.1.A1_at, BI403819, TRIM4	172.7	241.9	67.9	34.0	156.3	116.4	30.3	82.0	47.5	83.7
Ssc.15605.1.A1_at, CK452741, H1FX	907.4	592.9	559.5	778.8	1090.0	518.1	208.1	509.5	181.2	592.4
Ssc.28933.1.S1_at, AJ656592, HNMT	183.8	195.1	118.3	138.7	263.3	114.3	84.1	88.1	77.6	113.3
Ssc.5699.1.S1_at, BF710757, IQCK	710.5	551.7	864.6	508.5	661.0	420.0	356.7	505.4	125.3	361.3
Ssc.20.1.S1_at, AY450287.1, IL18	70.7	113.1	88.4	224.1	216.3	49.8	35.0	80.3	65.8	25.3
Ssc.30810.1.S1_at, CO956344, MITF	267.8	255.2	225.0	281.2	309.8	129.2	148.1	187.8	94.1	145.7
Ssc.19675.1.S1_at, CK457026, RACGAP1	154.6	121.6	147.5	296.1	324.7	121.9	120.9	192.0	63.3	134.3
Ssc.7043.1.A1_at, BF713147	508.7	504.5	310.4	793.9	663.7	345.6	282.7	400.3	228.7	345.4
Ssc.2801.1.S1_at, BP163360, RALGPS2	113.2	269.4	50.0	33.7	169.9	40.1	58.8	50.6	50.9	42.9
Ssc.3070.1.S1_at, BF712493, HIST1H2AK	520.9	419.3	355.7	991.8	725.8	313.5	155.9	337.9	179.0	352.3
Ssc.25607.1.S1_at, BX919614, PDAP1	212.8	92.0	179.9	131.4	114.4	360.8	350.1	133.4	169.3	149.4
Ssc.21302.2.S1_at, BE232076, ENPP6	481.5	932.6	406.1	246.1	578.3	27.3	303.1	299.7	121.9	381.0
Ssc.11089.1.S1_at, CK455718, RILPL2	574.6	455.9	605.1	481.2	479.5	342.8	261.7	322.2	274.8	288.2
Ssc.4177.1.A1_at, BI400924, WASF3	822.8	967.2	672.8	1255.4	957.6	635.9	486.1	544.3	409.0	331.9
Ssc.27177.2.S1_at, CK460274, ATP8A1	80.0	151.1	81.7	418.7	390.6	74.1	53.1	86.5	52.8	132.1
Ssc.7152.1.A1_at, BX925296, FIGF	1462.2	1341.0	918.7	1652.8	1787.6	753.9	638.7	930.4	417.5	1345.6
Ssc.5421.1.S1_at, CN154817, SYT11	1117.3	1448.8	1199.2	1885.8	2059.9	1080.8	676.2	1115.8	380.5	1395.9
Ssc.24500.1.S1_at, CK457922, MLF1IP	92.1	123.3	48.4	123.7	126.6	44.4	46.5	36.5	20.2	62.0
Ssc.1338.1.S1_at, CN160293, BLVRB	151.3	101.4	79.3	129.2	137.9	70.8	51.8	44.5	58.2	64.7
Ssc.10995.1.S1_at, CN163298, SNN	440.4	399.3	389.0	406.2	818.7	209.2	312.4	355.5	336.0	294.3
Ssc.27465.1.S1_at, CN160638, S100PBP	257.1	214.9	251.8	164.6	115.4	855.5	225.4	561.5	530.5	293.1
Ssc.27505.1.A1_at, CN165062, THEM2	306.2	257.8	234.9	284.9	282.9	159.2	153.4	188.6	106.4	211.8
Ssc.9260.1.A1_at, CK464473, NEK1	164.2	231.2	197.5	212.3	269.3	114.9	127.8	104.3	53.7	187.0
Ssc.3339.1.S1_at, CO943570, BCKDHB	272.2	292.6	204.6	291.0	478.4	174.2	84.3	141.6	65.6	230.5
Ssc.2842.1.A1_at, BQ598321, TMEM14A	165.8	198.9	160.7	261.5	263.0	147.8	87.3	142.9	90.2	166.3
Ssc.3714.1.S1_a_at, CK456589, BEX2	246.9	244.5	169.1	218.5	210.8	118.9	105.1	136.1	139.9	177.6
Ssc.8405.1.A1_at, BQ601342, PCDH15	61.5	93.1	64.2	103.5	107.4	84.9	26.3	36.3	38.9	53.3
Ssc.28780.1.A1_at, BM190323, KLHL7	278.3	304.3	167.0	455.8	374.9	165.2	136.9	147.2	75.8	249.3
Ssc.6159.1.A1_at, BF708614, TRAPPC9	84.6	95.0	84.3	114.5	98.0	58.0	41.7	70.4	56.9	57.0
Ssc.12129.1.A1_at, BI401037, ADD3	1345.1	904.4	743.9	1328.1	1220.7	694.6	529.3	1782.3	143.4	513.1
Ssc.4177.2.S1_at, BX925008, WASF3	401.0	545.5	291.4	365.1	465.3	306.8	270.0	152.1	147.0	106.2
Ssc.25044.1.S1_at, CK457564, CHD4	540.0	331.6	311.1	82.1	201.9	548.9	362.8	729.5	411.2	312.9
Ssc.5763.1.A1_at, CA780975, TMEM60	473.1	732.3	639.3	938.8	800.2	494.3	493.4	464.5	264.7	579.0
Ssc.2754.1.S1_at, BF713007, PRC1	207.9	162.3	197.0	257.2	231.4	141.2	86.5	115.4	71.9	136.0
Ssc.19151.1.S1_at, CN162742, FAM69B	116.0	480.5	131.4	492.1	373.0	168.0	107.0	225.6	93.4	186.0
Ssc.840.1.A1_at, Z83989, PKD2	96.4	105.6	48.7	38.1	86.3	24.4	37.8	37.2	20.8	59.7
Ssc.4174.1.S1_at, CN159189, ARHGAP12	90.8	60.9	74.3	58.5	131.9	58.4	64.5	54.7	38.4	41.9
Ssc.6996.1.A1_at, BF703515, PTK2	524.5	522.0	473.0	462.7	713.7	409.1	233.6	299.2	215.6	372.1
Ssc.27228.2.S1_at, CF178111, SEC63	181.1	281.7	169.4	78.1	173.2	462.9	300.7	131.1	256.1	176.9
Ssc.7039.1.A1_at, BI183564, NGFRAP1	635.8	580.8	405.2	1088.6	926.9	538.1	273.9	720.6	206.7	666.0
Ssc.24299.1.S1_at, CK454777, NCOA1	89.6	107.5	103.0	152.6	156.7	55.5	76.8	67.2	29.4	57.1
Ssc.24946.1.A1_at, CK459336, C7orf58	495.0	545.9	346.2	756.3	414.0	330.3	233.6	253.1	88.3	174.7
Ssc.5122.1.A1_at, BE749740, PIM2	108.7	104.2	99.3	76.6	88.8	130.2	258.2	262.6	330.5	161.9
Ssc.9914.1.A1_at, BQ604490, CKB	458.3	209.2	678.1	398.5	539.3	908.0	364.7	717.8	547.1	909.5
Ssc.7936.2.A1_at, BQ599817, INCENP	1190.5	1240.6	752.1	1835.2	1472.7	835.2	487.0	572.7	249.8	1015.9
Ssc.6923.1.A1_at, BF703306, KIF3B	243.0	444.8	286.1	781.4	428.5	307.2	199.5	360.4	106.7	409.3
Ssc.8375.1.A1_at, CF787952, RNF128	426.8	586.2	191.5	623.7	844.9	98.6	60.7	117.1	41.6	66.8
Ssc.5726.1.S1_at, BF703272, HERC3	217.8	188.5	154.9	322.8	390.7	179.2	169.5	141.6	68.4	217.8
Ssc.13183.2.S1_at, CF177814, RSBN1L	385.0	242.2	259.0	213.1	312.7	165.1	155.9	157.0	167.5	208.6
Ssc.3390.1.S1_at, CN069710, ADHFE1	119.9	93.9	84.5	164.0	159.0	87.4	52.1	69.0	51.4	53.9
Ssc.8663.1.A1_at, BF703355, PGRMC2	932.5	2704.8	1109.6	3118.4	3332.9	1832.8	952.1	918.5	447.9	1845.6
Ssc.18217.1.S1_at, CN160790, RSPO3	980.1	1211.9	702.2	2365.4	680.5	539.5	622.4	368.0	128.5	310.6
Ssc.11067.1.S1_a_at, CK461306, MEGF9	177.6	205.4	186.5	174.6	159.4	143.5	95.5	122.4	80.6	104.7
Ssc.13266.3.A1_at, BQ603334, SYCE2	254.4	394.3	169.6	405.3	345.6	118.9	137.3	98.1	42.1	92.4

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
951.5	1863.0	1116.4	958.6	978.6	869.2	591.2	217.5	1122.9	313.7	84.1	371.3	1.899329048	5.161732708
441.9	766.6	787.8	553.2	632.0	810.9	292.5	161.4	665.4	101.8	105.3	148.4	2.275027352	4.123187508
567.4	475.6	441.2	460.4	306.3	434.2	200.1	124.5	447.5	49.2	35.2	84.2	2.236241588	3.59393404
2553.5	2596.8	2398.1	1957.6	2933.2	1324.6	1151.6	761.7	2294.0	370.3	295.4	571.2	1.991912982	3.011719707
392.0	572.2	565.7	548.1	82.0	430.0	228.7	151.6	431.7	127.8	65.6	187.1	1.88781014	2.847405453
1585.8	2087.8	2317.4	1496.8	1553.3	981.7	298.3	601.1	1670.5	188.8	305.9	472.9	5.600330785	2.778831332
2276.9	1943.6	1871.6	1052.0	1280.9	2226.1	377.3	642.5	1775.2	242.2	344.2	502.0	4.705214518	2.762845255
142.0	290.8	151.5	372.7	91.9	123.2	134.6	72.0	195.4	83.7	33.7	110.7	1.451768728	2.713948319
956.0	1332.0	1191.5	924.4	1264.3	814.8	785.7	401.9	1080.5	221.2	192.1	209.7	1.375171817	2.688747325
306.4	366.6	245.3	179.0	212.1	218.5	179.8	95.5	254.7	56.3	17.1	69.5	1.415980872	2.667050691
896.0	1109.7	687.3	931.0	936.5	1001.8	659.3	353.7	927.1	140.6	141.1	139.6	1.406197858	2.620710126
197.2	49.9	138.4	224.6	77.5	109.4	142.5	51.2	132.8	72.5	22.3	67.9	0.932032931	2.592375748
356.3	394.1	302.6	431.6	361.7	322.5	267.8	141.0	361.5	31.4	33.9	46.9	1.349763505	2.563957062
437.7	283.1	279.4	288.9	302.6	294.9	208.9	126.5	314.4	94.0	45.8	61.0	1.505185894	2.486032047
872.3	1193.8	745.1	949.4	550.6	422.2	556.2	320.5	788.9	182.6	66.1	279.2	1.418272688	2.461159294
112.9	170.2	108.8	201.0	65.7	41.3	127.2	48.7	116.7	96.1	7.4	60.6	0.916771456	2.397246198
629.7	748.9	465.7	629.8	535.9	679.5	602.7	267.7	614.9	258.8	92.9	101.1	1.020269897	2.296864884
666.9	504.3	549.9	454.6	441.7	571.0	146.1	232.6	531.4	49.3	112.9	83.6	3.637234771	2.28460877
580.6	634.6	402.9	367.0	155.2	927.0	528.9	226.6	511.2	256.3	146.4	265.4	0.96652928	2.256031186
973.7	594.0	703.4	525.3	450.2	755.1	519.3	297.9	667.0	66.1	33.7	187.4	1.284423988	2.238537961
1108.6	1527.3	780.6	1147.5	1059.6	717.3	935.2	481.4	1056.8	215.4	117.7	291.1	1.13009182	2.195116041
256.1	169.4	124.5	180.0	184.9	131.6	224.4	79.7	174.4	167.3	32.6	47.3	0.777188605	2.187865864
2298.7	2109.8	1683.8	1894.3	1525.3	1151.1	1432.5	817.2	1777.2	334.6	349.2	414.8	1.240639646	2.174649013
2486.8	2382.2	1764.6	1886.2	1795.5	1789.8	1542.2	929.8	2017.5	416.2	400.2	327.3	1.308206891	2.169746049
74.8	87.8	83.9	140.5	93.8	64.8	102.8	41.9	90.9	33.5	15.3	26.3	0.884393438	2.169211196
174.5	98.0	100.7	176.9	103.4	100.6	119.8	58.0	125.7	29.1	10.4	38.8	1.048934513	2.166954023
897.5	647.7	623.1	548.5	513.2	686.7	490.7	301.5	652.8	184.4	56.6	135.9	1.330256222	2.165262483
1132.2	1198.2	1386.3	932.4	850.5	725.3	200.8	493.2	1037.5	60.4	249.5	244.9	5.167779106	2.103575291
389.9	387.5	309.9	341.4	236.3	389.9	273.3	163.9	342.5	27.5	39.8	61.4	1.252957245	2.089842161
207.5	389.3	252.6	171.5	213.0	238.2	214.9	117.5	245.4	39.1	47.9	75.8	1.141693811	2.087374511
285.9	308.8	235.9	332.2	271.1	283.9	307.8	139.2	286.3	101.9	67.1	32.8	0.930270341	2.056162022
310.2	300.7	207.8	252.0	230.2	259.2	210.0	126.9	260.0	49.9	35.9	39.6	1.238292536	2.048988705
281.0	353.8	275.6	257.0	173.2	323.7	218.0	135.5	277.4	31.5	27.3	62.1	1.272634122	2.046807359
97.6	116.2	53.8	138.8	149.4	29.9	85.9	47.9	97.6	21.7	22.8	47.4	1.135869987	2.036225838
315.2	501.8	286.2	326.1	233.9	218.2	316.1	154.9	313.6	108.1	62.6	101.8	0.992111203	2.024578168
153.0	94.8	110.2	88.7	73.3	163.5	95.3	56.8	113.9	12.4	10.2	36.5	1.195598936	2.005575117
2350.3	1810.0	1270.7	1120.6	1181.2	1072.7	1108.4	732.5	1467.6	269.9	620.5	508.6	1.324007915	2.003417333
439.6	582.7	284.3	493.5	334.7	218.7	413.7	196.4	392.3	96.8	86.8	137.0	0.948242518	1.996996233
1322.4	1069.7	983.2	775.5	677.9	792.0	293.3	473.1	936.8	170.0	168.2	237.7	3.193506966	1.980263251
1119.3	871.6	717.6	1037.7	928.7	776.0	716.7	459.2	908.5	174.6	116.8	152.9	1.267521463	1.978490643
206.4	292.4	178.1	181.5	276.2	143.1	211.2	110.2	213.0	35.8	30.3	59.1	1.008476984	1.932395644
414.0	407.8	232.5	348.0	180.3	225.9	318.6	156.0	301.4	184.0	55.2	101.3	0.946066123	1.93215812
53.9	91.5	40.8	73.1	85.2	68.5	75.0	36.0	68.8	29.9	15.3	19.0	0.917533102	1.91309987
124.0	111.4	100.7	92.3	99.8	61.2	83.3	51.6	98.2	30.1	11.1	21.2	1.179554915	1.904484942
480.0	828.8	424.5	569.5	532.9	553.1	539.2	305.9	564.8	101.5	84.3	139.8	1.047516599	1.84623431
526.4	340.7	425.5	538.8	265.4	791.6	176.7	265.5	481.4	72.2	128.7	185.0	2.724391624	1.812909543
813.1	1100.1	840.8	968.4	812.1	676.2	727.5	481.1	868.5	275.7	230.8	146.7	1.193811344	1.805284164
130.8	113.5	109.7	103.0	91.9	69.3	121.9	57.2	103.0	30.7	17.7	20.9	0.845367028	1.801282051
463.8	260.3	371.7	356.1	770.7	108.0	511.5	216.0	388.4	156.7	90.5	222.8	0.75943015	1.798302469
547.2	412.3	398.2	268.8	348.8	471.6	95.5	228.7	407.8	12.9	81.5	96.4	4.269437465	1.783350825
1575.5	605.0	1435.6	569.1	1849.4	1309.7	456.7	689.4	1224.1	173.6	236.0	525.1	2.680323202	1.775477938
1411.2	1593.9	758.0	956.7	906.2	1050.4	1298.2	632.1	1112.7	397.5	299.7	321.7	0.857122316	1.760319771
525.5	587.9	605.1	430.5	348.9	369.3	436.8	276.6	477.9	211.6	122.9	110.7	1.094117288	1.727520305
277.4	33.5	66.9	284.6	105.6	29.5	534.6	77.0	132.9	243.0	30.4	118.0	0.248618957	1.727087665
378.9	202.7	314.7	292.6	182.1	236.4	254.9	155.3	267.9	98.5	55.7	74.5	1.050835491	1.725048294
342.1	353.5	241.2	321.8	282.4	216.4	282.4	170.8	292.9	67.8	21.7	55.8	1.037181303	1.714670413
85.5	162.9	64.3	131.9	154.0	46.1	124.3	62.8	107.5	36.4	15.6	48.9	0.864719137	1.712077757
2532.9	2126.5	1489.0	2731.7	1704.8	1644.6	2239.6	1199.4	2038.3	1136.8	617.2	510.1	0.910079298	1.6994197
832.3	1159.7	519.4	478.3	243.1	774.9	1188.0	393.8	668.0	693.5	194.6	322.1	0.562238009	1.696165566
220.2	196.4	202.3	173.6	151.1	164.6	180.7	109.3	184.7	16.9	24.4	25.9	1.022136137	1.689226267
184.2	214.5	109.2	252.6	134.7	94.4	313.8	97.8	164.9	100.2	35.8	62.5	0.52553318	1.687124932

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.27009.1.A1_at, CN164842, MAP1B	41.6	35.9	57.1	30.1	81.0	85.6	104.8	107.5	32.1	57.9
Ssc.24360.1.S1_a_at, CN160303, SLC17A5	492.6	611.4	490.7	666.7	746.2	374.3	508.1	418.1	192.3	361.7
Ssc.6789.1.A1_at, CK464556	245.1	219.9	252.6	463.6	380.8	205.8	177.3	326.8	73.3	246.8
Ssc.13397.1.S1_at, CK464886, ARL3	1140.2	1034.1	1287.6	1008.7	928.2	1849.5	1602.0	1268.8	1841.2	1900.9
Ssc.5609.1.A1_at, BF704192, NKAIN2	442.1	427.6	316.3	416.3	574.5	205.8	224.1	341.0	132.9	247.1
Ssc.2939.1.S1_at, BF703829	565.4	479.7	477.8	497.6	447.4	358.1	272.6	348.5	271.5	310.8
Ssc.1012.1.S1_at, BQ600156, ZNF277	1453.1	1210.3	959.6	1313.8	1622.3	1005.3	815.9	796.3	636.2	860.2
Ssc.30704.3.A1_at, CO991344, TSHZ1	260.4	248.7	177.9	383.0	188.9	108.0	120.0	245.4	107.1	152.4
Ssc.9461.1.A1_at, BF710595, ERRFI1	71.1	81.8	87.2	101.6	42.9	200.9	70.4	185.5	105.8	79.9
Ssc.29302.1.A1_at, CO953488, SLIT3	66.7	98.9	85.2	105.6	69.8	90.4	57.1	56.9	34.9	40.8
Ssc.15582.1.S1_at, CK450991, ARHGAP18	127.8	98.5	134.1	198.1	307.5	71.4	66.5	108.1	55.2	74.7
Ssc.30581.1.A1_at, CO994287, CDC14A	78.7	106.3	79.9	139.3	116.9	105.4	45.3	76.2	59.1	52.4
Ssc.4498.1.S1_at, BX921814, MED29	307.4	239.2	234.1	270.2	405.8	211.2	150.4	218.9	130.9	204.8
Ssc.888.1.A1_at, CN163063, ERRFI1	507.8	557.3	591.8	396.3	468.4	811.0	1210.4	810.6	1016.8	576.3
Ssc.761.1.S1_at, NM_214247.1, NR4A3	63.2	73.1	136.7	177.5	111.5	189.1	148.5	237.5	93.9	183.0
Ssc.14400.1.A1_at, CK457556, SGMS1	809.3	1102.0	512.1	725.1	821.2	475.8	490.9	493.7	375.2	507.2
Ssc.7243.1.A1_at, CO945718, CXCL12	31.2	70.4	21.5	76.0	35.4	51.4	12.7	16.1	19.3	17.7
Ssc.7546.1.A1_at, BQ599193, ARHGAP11A	152.1	100.1	74.2	130.4	103.6	45.2	105.2	80.2	75.6	46.8
Ssc.12523.1.A1_at, BI402693, CLIC4	760.0	599.8	508.3	289.9	404.2	2192.5	774.0	516.6	1134.9	793.3
Ssc.3192.1.A1_at, BI401776, FAM35B	134.0	150.6	84.5	147.7	109.6	68.1	72.0	53.7	78.2	118.8
Ssc.3823.1.A1_at, CB478894, CADM1	1066.0	1137.3	688.4	863.6	1141.2	221.5	330.8	794.2	359.9	290.8
Ssc.10232.1.A1_at, BI400288, MYLIP	2743.0	2394.8	1922.5	2768.3	2172.2	919.0	960.8	1588.8	1567.9	1267.2
Ssc.25149.1.S1_at, BI346240, MAGI3	333.2	174.5	248.0	470.8	182.8	125.2	121.4	209.1	67.9	169.7
Ssc.1056.1.A1_at, CO994056, PRKAR2B	458.4	645.0	544.2	1312.8	644.5	479.1	422.2	739.9	182.0	460.8
Ssc.10727.1.A1_at, CO940842, RBL2	1546.6	1824.3	839.6	2224.2	2002.9	1386.2	928.1	946.9	423.1	1564.8
Ssc.4361.2.S1_a_at, CK451362, WDFY2	236.3	205.5	198.3	159.0	287.8	209.8	105.6	133.9	82.4	185.9
Ssc.2289.1.S1_at, AW785855, SCAPER	232.4	252.4	214.3	289.7	261.3	146.9	159.0	189.3	115.4	212.6
Ssc.20151.1.S1_at, BI399237, CADM1	406.0	618.8	463.2	521.7	713.1	161.8	214.4	404.3	166.9	193.7
Ssc.22476.1.A1_at, CF795151, TXNDC16	89.0	73.2	48.4	60.2	76.8	67.1	40.0	73.0	16.3	30.1
Ssc.4771.1.S1_at, CN160335, PPP1R16B	95.1	101.0	61.7	70.5	83.6	148.7	111.5	101.3	138.0	132.1
Ssc.1553.1.S1_at, CN152986, CDC2L6	414.6	452.8	363.6	1008.2	712.6	427.9	250.6	306.6	68.5	348.5
Ssc.8415.1.A1_at, BQ601369, BACE1	422.1	410.9	403.7	504.7	351.8	272.0	182.4	375.1	157.5	328.3
Ssc.7777.1.A1_at, CO956583, TMTC4	1059.9	1199.9	821.6	1836.0	1129.2	724.0	506.3	956.5	389.5	1121.5
Ssc.7373.1.A1_at, CF789103, PPAPDC3	232.0	308.6	224.7	450.2	431.9	215.3	154.1	185.5	169.4	230.5
Ssc.8349.1.A1_at, CD572266	23.1	59.4	26.8	69.3	35.6	39.4	17.3	19.1	16.0	20.3
Ssc.5243.1.A1_at, BI404769, PTCH1	434.7	714.1	404.8	704.8	808.6	334.2	494.6	383.2	264.6	372.9
Ssc.8275.1.A1_at, BI184073, RNF13	720.1	625.6	341.5	804.8	963.8	226.9	390.6	373.1	272.4	567.1
Ssc.7136.1.A1_at, CO953639, CDC2L6	327.5	418.8	216.7	713.0	585.7	310.7	175.0	292.6	50.2	310.7
Ssc.9380.1.S1_at, CF175279, GADD45B	736.2	679.7	741.2	219.6	549.4	1873.6	677.2	522.5	616.7	705.4
Ssc.1013.1.A1_at, NM_214300.1, MGST1	116.6	160.4	108.6	137.9	305.3	72.7	63.6	80.7	57.5	100.3
Ssc.31102.1.A1_at, CO989361, SCIN	286.9	372.6	244.8	418.5	570.2	94.8	86.5	144.8	80.4	54.2
Ssc.5129.1.S1_at, CN154490, MAD2L1	337.3	355.8	306.5	389.1	485.3	250.8	276.1	229.0	233.3	254.6
Ssc.9056.1.A1_at, CF359981, GRIP1	237.0	291.1	109.8	365.2	436.1	103.0	106.9	149.0	79.5	130.0
Ssc.10005.1.S1_at, CN154303, SENP6	122.5	107.7	51.7	19.7	83.3	152.7	129.2	92.1	132.5	76.4
Ssc.25145.1.S1_at, CK465844, POT1	152.6	179.7	92.7	177.7	204.5	77.6	85.1	107.2	41.9	117.2
Ssc.6092.1.A1_at, CN166399, NCAM1	632.4	868.4	612.4	1198.4	952.8	422.2	243.1	706.0	363.6	585.4
Ssc.14232.1.S1_at, BP461945, SYNCRIP	238.4	264.9	184.3	46.1	235.6	463.7	419.3	146.9	403.5	135.4
Ssc.21582.1.S1_at, CO954945	135.9	724.3	140.9	611.4	488.4	160.8	53.8	345.9	291.9	313.0
Ssc.9958.1.A1_at, BI399442, IQCK	283.2	202.2	308.8	345.0	204.9	125.7	118.9	208.2	91.1	176.5
Ssc.24020.1.S1_at, CK455702, SGCD	104.0	119.7	105.7	119.2	78.1	85.7	64.9	43.1	46.6	69.1
Ssc.9762.1.A1_at, BI398829, PDE3A	266.3	422.6	216.3	552.3	581.6	177.1	101.8	195.3	82.8	222.0
Ssc.29706.1.A1_at, CO945153, ATAD2	175.0	204.7	104.7	229.5	149.2	132.1	130.7	119.1	90.9	93.8
Ssc.2132.1.S1_a_at, CK464544, RPS6KA5	156.1	233.0	104.1	385.9	596.4	61.3	169.0	278.6	90.5	189.0
Ssc.18929.1.S1_s_at, CF366027, RNF128	1582.8	2073.0	761.9	3585.5	2444.8	358.6	191.5	455.1	126.6	249.1
Ssc.30704.1.S1_at, BP463139, TSHZ1	676.4	655.5	566.0	588.2	705.7	268.3	448.5	420.0	242.4	379.5
Ssc.31120.1.A1_at, CF180939, NCOA1	293.8	275.7	252.5	540.8	407.1	193.1	137.9	316.3	93.9	282.6
Ssc.3518.1.S1_at, BF702996, IDH1	300.4	293.9	261.2	405.0	461.1	230.8	178.6	291.6	98.6	286.5
Ssc.28921.1.S1_at, CN165359, MAGI3	570.7	547.6	563.8	1176.1	394.0	301.4	327.6	315.2	119.2	352.1
Ssc.12944.1.A1_at, CN154203, RPA3	1354.8	1551.4	1179.7	2272.9	2225.1	974.9	997.6	985.6	629.1	1237.3
Ssc.27276.1.A1_at, CN153125, SNORA32	65.4	55.5	46.1	42.1	41.1	123.7	64.7	89.9	79.7	47.1
Ssc.9398.1.A1_at, BF710441, SSBP2	51.7	79.9	69.0	123.0	113.8	71.1	34.7	85.3	28.0	60.1

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
170.1	89.8	93.0	63.2	270.1	96.1	49.1	77.6	130.4	20.5	32.2	77.2	2.653303487	1.680630747
789.4	778.4	543.7	651.8	515.1	451.5	601.5	370.9	621.7	111.2	115.2	141.4	1.033465221	1.676058237
421.2	459.9	289.1	313.1	289.9	297.9	312.4	206.0	345.2	105.1	93.1	75.4	1.104940248	1.675647249
3197.7	3012.4	2785.4	2365.2	2167.8	3327.4	1079.8	1692.5	2809.3	138.7	263.6	462.6	2.601797313	1.659881751
361.4	501.9	318.3	471.3	415.2	223.6	435.4	230.2	382.0	92.2	75.3	103.0	0.877319919	1.659353549
533.8	667.9	570.5	482.1	330.0	496.2	493.6	312.3	513.4	44.0	40.8	111.8	1.040189365	1.643985484
1499.6	1788.7	906.9	1368.1	1302.7	1205.5	1311.8	822.8	1345.3	250.4	132.5	294.8	1.025483679	1.635005712
251.7	279.1	213.8	258.9	265.5	166.5	251.8	146.6	239.3	81.7	58.2	41.9	0.950234332	1.63221449
108.3	140.5	326.7	78.3	384.3	219.4	76.9	128.5	209.6	22.0	60.7	123.8	2.724692321	1.630998703
81.2	113.4	68.3	46.6	144.9	93.1	85.2	56.0	91.3	17.2	21.6	34.6	1.070506804	1.628882542
199.2	82.2	77.7	160.7	130.2	83.9	173.2	75.2	122.3	83.4	19.8	50.0	0.70621632	1.626984127
98.6	131.4	104.9	114.8	73.9	135.6	104.2	67.7	109.9	25.7	24.0	22.8	1.05418026	1.623325453
304.4	403.5	254.4	373.3	213.2	218.0	291.3	183.2	294.5	70.4	39.8	80.3	1.01073202	1.606999927
1385.0	714.1	1413.1	401.1	2574.9	1998.3	504.3	885.0	1414.4	76.5	239.6	800.7	2.804601576	1.598174806
281.3	215.5	207.9	184.8	317.9	426.3	112.4	170.4	272.3	46.9	53.3	90.5	2.422449585	1.597906886
1045.7	909.7	642.9	469.4	591.1	820.1	793.9	468.6	746.5	212.2	53.4	216.0	0.940226382	1.593143532
16.5	56.6	31.3	38.5	70.3	9.0	46.9	23.4	37.0	24.6	15.8	23.4	0.789623312	1.579920364
146.9	93.8	113.8	89.2	154.1	69.6	112.1	70.6	111.2	29.9	25.1	33.6	0.992445872	1.575542965
2685.5	1541.5	1196.7	965.8	1137.6	2660.3	512.4	1082.3	1697.9	180.4	658.4	778.1	3.313363516	1.568846673
160.8	155.4	90.6	103.9	107.9	114.6	125.3	78.2	122.2	28.0	24.4	28.9	0.97541507	1.56345957
669.6	1006.2	718.7	519.2	300.4	515.6	979.3	399.4	621.6	197.9	226.7	238.6	0.634756118	1.556220375
2078.7	3394.1	1917.4	1570.4	1871.7	921.5	2400.2	1260.7	1959.0	365.1	319.7	813.7	0.816181699	1.553822887
232.3	319.8	212.0	223.5	207.5	94.3	281.9	138.7	214.9	123.3	53.4	72.1	0.762435252	1.549834127
926.2	788.0	690.9	571.4	757.6	508.3	721.0	456.8	707.1	339.9	198.4	151.9	0.980702192	1.547869235
2073.6	2547.3	1009.6	1547.2	1201.0	1335.9	1687.5	1049.8	1619.1	535.0	446.2	583.1	0.959455295	1.542264388
306.2	195.3	190.5	261.4	182.7	188.3	217.4	143.5	220.7	48.0	53.5	51.0	1.015426135	1.537997027
262.6	336.8	227.5	247.0	195.8	246.9	250.0	164.6	252.8	28.7	37.7	47.1	1.010985788	1.535268869
372.2	505.4	414.6	333.1	165.6	303.8	544.6	228.2	349.1	122.7	100.7	114.2	0.641098624	1.529737388
84.3	70.9	63.4	50.2	68.9	77.6	69.5	45.3	69.2	15.6	24.2	11.8	0.995636747	1.527961737
261.5	232.0	210.8	147.1	131.8	174.2	82.4	126.3	192.9	16.4	19.5	50.5	2.341587764	1.527074098
484.1	624.0	340.1	468.3	353.7	296.4	590.4	280.4	427.8	269.6	135.0	121.5	0.724586128	1.52544992
473.6	560.3	348.3	310.7	351.9	344.2	418.6	263.1	398.2	55.2	92.9	97.1	0.951095611	1.513596391
1124.1	1778.3	856.8	989.4	1110.7	847.5	1209.3	739.6	1117.8	378.1	304.2	344.7	0.924321106	1.511439234
362.9	309.5	195.2	395.2	206.4	258.7	329.5	191.0	288.0	107.2	31.7	82.1	0.874054065	1.508081972
16.9	48.7	19.5	15.2	87.0	14.9	42.8	22.4	33.7	20.5	9.6	29.1	0.786647993	1.503122212
727.0	744.8	407.4	636.8	447.2	362.6	613.4	369.9	554.3	181.7	83.8	169.0	0.903651777	1.498513112
728.9	379.1	738.2	787.2	259.3	396.4	691.2	366.0	548.2	231.6	131.5	228.5	0.793135212	1.497686829
387.3	427.4	257.0	481.2	285.9	200.4	452.3	227.8	339.9	198.7	114.3	108.7	0.751352228	1.491690075
1443.8	1741.8	1159.7	1443.0	874.0	1199.9	585.2	879.1	1310.4	218.5	560.4	298.9	2.239100965	1.490611397
152.7	113.7	77.9	132.9	52.3	137.6	165.8	75.0	111.2	80.6	16.7	38.7	0.670748874	1.483235503
248.0	11.0	109.0	218.5	68.9	163.3	378.6	92.1	136.5	127.1	33.1	90.5	0.360406762	1.480898633
407.3	388.2	307.4	340.3	355.3	410.9	374.8	248.8	368.2	68.6	18.8	41.0	0.982479545	1.4802755
191.0	306.4	112.7	172.1	113.4	106.5	287.8	113.7	167.0	124.8	26.7	76.8	0.580241338	1.469182501
188.7	157.8	197.2	204.2	63.1	215.5	77.0	116.6	171.1	41.8	31.3	56.4	2.222438729	1.467518728
130.0	167.0	101.6	133.9	117.7	104.7	161.4	85.8	125.8	42.6	29.3	24.0	0.779340106	1.466394716
706.6	977.2	624.9	754.0	584.9	431.9	852.9	464.1	679.9	242.9	183.0	183.4	0.797200857	1.465148185
551.1	323.7	451.6	342.0	299.0	768.6	193.9	313.8	456.0	87.6	159.2	180.0	2.352212937	1.453340133
146.7	57.9	90.4	300.1	42.4	1376.6	420.2	233.1	335.7	270.4	122.4	518.4	0.798903644	1.44020651
215.3	243.8	191.9	151.0	397.0	42.2	268.8	144.1	206.9	63.5	47.3	116.7	0.769535997	1.435776421
96.0	102.7	87.4	74.8	150.9	18.2	105.3	61.9	88.3	16.9	17.4	43.1	0.838554522	1.427494075
228.1	327.8	189.0	238.7	196.9	153.8	407.8	155.8	222.4	164.3	60.5	59.8	0.545297762	1.427364142
159.0	168.9	140.6	170.1	175.0	156.1	172.6	113.3	161.6	48.6	19.8	12.5	0.936256903	1.4261972
171.2	438.7	188.2	248.1	152.3	140.1	295.1	157.7	223.1	199.2	85.9	112.2	0.75601491	1.414890918
816.1	105.9	213.3	741.1	351.7	114.7	2089.6	276.2	390.5	1046.9	131.4	314.3	0.186861919	1.413812248
536.1	645.4	439.7	487.5	576.4	297.2	638.4	351.7	497.1	59.2	91.8	121.0	0.778635879	1.413117644
306.5	356.7	253.3	328.2	280.0	209.2	354.0	204.8	289.0	120.2	94.1	53.2	0.816383223	1.411327082
312.1	407.5	256.8	328.4	319.6	200.4	344.3	217.2	304.1	84.7	80.7	70.1	0.883286865	1.400116625
487.0	591.6	303.5	399.1	298.6	287.0	650.4	283.1	394.5	302.7	93.5	123.7	0.606461267	1.393382786
1439.6	1392.6	1202.0	1453.2	1091.8	1419.3	1716.8	964.9	1333.1	503.6	217.1	149.8	0.776502134	1.381576675
75.8	120.3	154.4	99.4	113.3	103.1	50.0	81.0	111.1	10.3	28.8	26.1	2.21922462	1.370649222
73.8	105.3	59.3	95.0	85.5	39.6	87.5	55.8	76.4	30.1	24.2	24.2	0.873532998	1.368493314

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.14282.1.A1_at, BQ601688, LRP11	244.1	437.1	135.8	1000.7	562.5	116.4	69.3	249.7	57.9	181.4
Ssc.18240.1.S1_at, AW430762, MOAP1	173.0	92.7	80.8	70.6	168.7	46.8	73.8	45.9	59.8	75.4
Ssc.5730.2.A1_at, BQ605161, KPNA1	1553.9	1401.0	1316.1	1103.8	1120.1	2025.4	2072.0	1867.2	2468.3	1343.9
Ssc.21960.1.S1_at, BX666579, FUSIP1	213.6	268.1	164.2	101.3	224.9	340.7	313.9	279.1	398.6	236.2
Ssc.7529.1.S1_at, CO952434	373.8	439.1	433.1	467.3	450.4	275.4	207.9	259.2	223.3	337.9
Ssc.16940.1.A1_at, CK452154, KAT2B	355.2	636.4	408.5	686.8	618.2	438.0	249.0	225.8	204.4	308.4
Ssc.31207.1.S1_at, BI327158, TMPO	65.6	38.1	60.0	70.2	52.8	29.9	62.8	28.4	23.0	45.4
Ssc.27239.1.S1_at, CF792291, KLF12	596.9	362.4	361.2	697.4	529.0	234.2	173.0	436.0	183.3	266.9
Ssc.22133.1.A1_at, CF787921	141.7	88.8	105.7	219.1	110.2	83.5	50.3	76.7	28.0	174.5
Ssc.6969.1.A1_at, CN167055, MDM1	52.7	58.6	34.7	87.0	90.6	17.2	38.7	51.6	21.2	49.7
Ssc.16038.1.S1_at, AB012858.1	352.2	615.1	306.3	662.1	326.1	210.9	96.1	144.8	144.3	380.8
Ssc.2742.1.S1_at, BF702440, C11orf67	534.4	585.1	475.4	779.6	590.8	337.0	250.2	437.7	245.4	464.7
Ssc.17250.1.S1_at, BM189976, QDPR	347.0	364.7	224.0	367.8	345.7	300.7	145.5	152.6	117.1	127.4
Ssc.12492.2.S1_at, BI402572, SORT1	2756.8	2568.2	2085.9	3232.6	2835.8	1378.4	1496.5	2286.8	1250.7	2228.3
Ssc.7141.1.A1_at, BF702664, CNN3	97.0	96.3	88.2	170.1	164.7	51.1	85.5	93.2	82.4	79.3
Ssc.29185.1.A1_at, CO951446, ITGA8	1818.3	479.0	1035.8	3617.3	1716.5	1188.2	487.9	939.9	389.1	1405.6
Ssc.31175.1.S1_at, CO993891, AUTS2	495.3	170.5	456.5	815.3	433.4	426.3	330.2	417.5	150.5	136.2
Ssc.7157.1.A1_at, BQ598555, HBD	3550.8	1268.4	1589.0	2455.1	4018.6	4703.8	1097.8	2816.2	3064.0	12135.5
Ssc.13450.1.A1_at, CF368821, ERMN	80.0	76.7	47.0	108.5	51.3	52.3	21.3	53.3	41.7	46.8
Ssc.20816.1.S1_at, BP459811, NCAM1	570.5	625.6	491.4	686.2	729.3	347.5	254.5	690.5	347.5	423.3
Ssc.2510.1.S1_at, CF180007	514.4	680.6	414.7	706.9	883.1	423.2	384.5	342.7	218.0	433.4
Ssc.101.1.S1_at, NM_214023.1, SPP1	2883.4	2292.4	1854.0	1076.0	1893.1	570.6	1430.6	1098.0	1612.4	396.0
Ssc.10025.1.S1_at, BF711030	854.4	743.1	809.8	337.2	801.0	350.0	739.5	264.2	398.1	390.5
Ssc.5509.2.S1_at, BP437179, ARL4A	605.8	611.2	434.6	485.3	560.6	312.4	249.9	333.6	234.7	314.1
Ssc.31052.1.A1_at, CK460889, FAM63B	436.5	385.7	422.5	514.3	399.7	280.1	239.0	225.7	217.2	343.8
Ssc.30550.1.A1_at, CO993779, COL11A1	157.9	127.7	66.2	222.1	195.2	51.2	42.1	97.6	42.3	42.4
Ssc.12622.1.A1_a_at, CF180494, AUH	356.3	349.2	386.8	327.1	373.9	237.2	328.1	195.3	98.7	278.9
Ssc.31164.1.S1_at, CO987486, MYO1B	146.9	52.4	80.8	50.9	80.0	157.1	208.4	108.1	154.0	129.7
Ssc.22427.1.A1_at, CK466902	166.8	138.1	286.9	84.5	76.3	220.5	541.0	243.4	432.5	119.4
Ssc.7785.1.S1_at, CK456652, TMEM123	1250.0	1181.4	1088.2	2051.9	1161.5	1075.1	836.7	853.4	714.8	848.8
Ssc.1692.1.A1_at, BF709272, ADAM12	506.4	583.2	395.4	405.5	463.4	260.4	211.4	276.0	109.1	251.3
Ssc.2364.1.S1_at, CF364972, PER3	366.4	480.2	245.4	310.2	249.4	191.2	256.7	199.1	159.1	252.6
Ssc.29746.1.A1_at, CO945222, TSHZ1	1016.6	933.0	817.5	1349.7	865.6	503.1	687.9	1012.1	456.8	536.6
Ssc.29424.1.A1_at, CO955169, PLEKHA5	83.9	107.9	100.2	130.3	103.0	69.2	59.8	81.2	37.3	72.1
Ssc.11220.1.S1_at, BG382265, TGIF2	111.6	115.8	121.6	83.2	111.3	117.7	184.6	202.0	230.9	122.2
Ssc.6928.1.A1_at, CO989436, ALDH1A1	145.3	286.9	286.7	746.3	280.4	383.4	153.1	257.4	89.0	150.1
Ssc.24342.1.S1_at, CK455917, SLIT2	498.3	466.0	386.5	583.2	823.3	146.9	234.3	152.3	76.8	533.6
Ssc.5491.1.S1_at, CA780426, PTGES3	1173.8	1834.7	567.9	1245.6	1984.5	556.0	448.1	756.9	295.5	1040.7
Ssc.6339.1.A1_at, BI181680, DHTKD1	165.5	251.1	138.6	240.7	398.7	51.4	91.3	85.1	59.3	84.2
Ssc.12492.1.A1_at, CN167016, SORT1	1065.7	1373.6	1024.2	1425.4	1433.4	661.1	558.9	844.7	609.1	1160.9
Ssc.18240.2.A1_at, CF175230, MOAP1	247.3	145.9	213.4	210.8	289.9	112.2	93.8	58.9	141.6	122.2
Ssc.3706.1.S1_at, NM_214127.1, SOD2	271.0	413.6	461.8	236.1	444.6	442.0	710.4	378.2	955.2	491.9
Ssc.12393.1.A1_at, BX915086, CABC1	596.4	564.5	232.7	664.0	598.4	222.5	163.9	319.0	111.3	278.2
Ssc.5318.1.A1_at, CF360511, BBX	268.3	264.4	280.8	366.8	219.7	132.6	198.4	282.6	85.3	203.7
Ssc.7139.1.S1_at, BX925457	245.7	361.7	286.1	444.4	568.0	231.7	248.8	244.5	142.0	221.0
Ssc.210.7.S1_x_at, AB016750.1	2021.4	671.3	984.7	839.8	3597.4	400.5	1505.8	836.4	1624.1	799.2
Ssc.22874.1.S1_at, CN158395, LBR	432.7	423.3	440.0	486.4	556.4	418.0	172.9	430.4	173.6	349.2
Ssc.808.1.S1_at, BQ602208, PCCA	366.2	367.5	293.5	547.7	435.2	276.2	123.1	267.5	83.7	241.3
Ssc.6629.1.S1_at, CF789179, HERC1	975.6	958.1	814.3	1568.2	1168.8	670.5	585.5	878.0	540.3	950.0
Ssc.2381.1.A1_at, BI402402, S100A9	72.7	37.9	135.4	68.1	87.4	188.5	67.2	129.6	114.2	257.3
Ssc.13529.1.A1_at, BQ602610, ZNF711	108.2	125.8	60.8	124.9	150.7	43.3	46.2	78.0	23.2	57.5
Ssc.8620.2.S1_at, BX924744, CLEC1A	110.2	127.3	82.0	95.8	292.7	36.5	71.0	47.8	52.0	104.3
Ssc.1578.1.S1_at, BX665001, GGA2	386.3	498.7	421.0	478.6	625.5	292.9	311.7	408.7	202.6	317.6
Ssc.6482.1.A1_at, BQ602535, GMCL1	421.5	488.8	352.6	752.5	643.1	269.8	343.9	357.0	337.0	361.4
Ssc.6343.1.S1_at, BQ597891, CNTN1	137.4	170.0	345.4	223.0	54.7	120.9	58.4	59.3	74.9	221.9
Ssc.20954.2.S1_a_at, BP154520, MRPL3	317.2	557.9	318.3	166.0	407.3	638.4	706.3	201.4	705.5	402.9
Ssc.27680.1.S1_at, AW480248, GRIA1	111.3	157.7	67.1	83.4	124.3	54.4	85.4	59.0	53.4	79.1
Ssc.167.2.S1_a_at, AF372455.1, FCGR3B	567.8	582.1	342.7	749.8	1315.0	333.4	250.4	323.5	204.2	292.5
Ssc.25282.1.S1_at, BX914285, SH3BP5	2343.3	2190.5	1747.4	2061.9	2430.3	1135.8	1579.8	1560.1	1086.7	1713.5
Ssc.17772.1.S1_at, AJ577089.1, FGF2	93.0	82.8	84.1	54.8	121.7	154.6	152.1	57.7	265.6	135.5
Ssc.18003.1.A1_at, CN154900, C22orf39	347.2	404.1	221.8	387.6	494.5	181.5	178.4	174.3	142.3	311.6
Ssc.4989.1.A1_at, CN165749, CTH	234.8	315.5	127.6	330.5	364.2	168.1	152.9	144.8	196.5	112.1

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
124.1	353.6	134.2	278.4	87.6	128.2	476.0	134.9	184.4	336.8	80.5	106.0	0.387257373	1.366162739
115.8	76.2	74.5	91.7	91.8	42.8	117.2	60.3	82.1	49.7	14.1	24.3	0.701035621	1.361175561
3437.4	2569.3	2849.9	2102.6	2479.9	2511.1	1299.0	1955.4	2658.4	190.9	407.2	450.3	2.046503154	1.359527998
447.1	487.1	435.2	329.0	352.6	505.6	194.4	313.7	426.1	63.9	61.5	71.3	2.19164695	1.358304112
445.3	472.7	280.7	306.5	302.1	307.1	432.7	260.7	352.4	35.4	50.9	83.6	0.814345797	1.351537931
389.6	581.2	257.4	513.0	366.7	198.2	541.0	285.1	384.4	148.7	93.9	145.9	0.71041736	1.3480289
58.0	50.6	29.4	57.9	57.1	53.5	57.3	37.9	51.1	12.6	16.2	11.0	0.890884781	1.347845207
442.0	411.9	269.4	252.0	493.4	221.2	509.4	258.7	348.3	147.4	106.2	114.5	0.683805149	1.346515644
64.6	286.9	58.1	87.3	75.1	95.0	133.1	82.6	111.2	51.7	55.9	87.2	0.83521162	1.345843422
49.2	41.8	53.0	38.1	38.1	66.3	64.7	35.7	47.8	23.7	15.9	10.9	0.737793572	1.338284753
398.6	233.8	177.5	342.4	50.2	364.4	452.4	195.4	261.2	171.6	111.4	133.0	0.577305686	1.336626062
596.1	541.6	417.4	464.4	369.6	390.8	593.1	347.0	463.3	114.2	102.3	89.3	0.781230679	1.335206532
330.1	237.9	246.5	146.5	142.5	242.9	329.8	168.7	224.4	60.0	75.1	70.7	0.680329857	1.330487371
2461.1	3355.2	2285.7	1749.5	1836.7	2058.8	2695.9	1728.1	2291.2	418.3	491.5	585.7	0.849883401	1.325799222
62.2	137.4	134.2	115.0	123.6	50.4	123.3	78.3	103.8	40.5	16.1	37.8	0.842122343	1.325670498
1248.1	1095.1	1108.8	1069.9	1956.7	528.7	1733.4	882.1	1167.9	1185.0	438.6	459.5	0.673760706	1.323920617
444.0	398.0	327.5	125.5	721.3	304.1	474.2	292.1	386.7	229.7	141.0	196.9	0.815548995	1.323794528
7368.2	12088.3	11243.3	3435.7	1296.7	2263.2	2576.4	4763.5	6282.6	1196.9	4314.7	4660.7	2.438524855	1.318908245
67.3	114.9	49.8	32.1	41.3	33.8	72.7	43.1	56.5	24.8	13.0	31.3	0.777624943	1.312287218
553.7	679.7	566.5	552.9	446.4	446.1	620.6	412.7	540.9	94.0	166.4	87.3	0.871549039	1.310723921
578.6	642.5	399.2	490.4	433.3	279.7	639.9	360.4	470.6	181.5	87.2	130.0	0.735407486	1.305962556
1622.3	184.1	492.4	2919.0	1420.5	1342.0	1999.8	1021.5	1330.1	661.9	528.4	962.6	0.665098161	1.302030308
456.6	387.2	416.2	560.9	600.1	921.5	709.1	428.5	557.1	211.6	181.8	196.7	0.78562027	1.300199163
380.3	454.0	252.2	400.0	250.1	515.3	539.5	288.9	375.3	77.3	43.7	107.0	0.695675008	1.298943264
396.2	356.1	366.2	298.8	213.2	401.5	431.7	261.2	338.7	50.2	52.1	71.6	0.784422724	1.296778476
92.3	108.3	53.5	55.7	73.2	45.2	153.8	55.1	71.4	60.7	24.1	24.7	0.463962207	1.294750847
289.4	416.3	213.5	342.5	300.2	203.7	358.7	227.6	294.3	23.0	87.3	80.0	0.820461347	1.292684355
276.6	226.5	172.2	91.9	191.6	213.2	82.2	151.5	195.3	38.9	37.5	61.9	2.376317924	1.28966944
648.2	179.7	519.9	207.7	358.9	485.1	150.5	311.4	399.9	85.0	171.1	184.6	2.656900523	1.284418893
1334.2	1189.4	825.7	1087.0	949.2	1284.8	1346.6	865.8	1111.7	398.5	130.3	197.1	0.825573048	1.284093359
264.7	384.5	298.9	213.1	279.8	261.9	470.8	221.6	283.8	77.3	67.3	57.0	0.602864749	1.280529989
278.4	444.6	208.7	366.9	175.2	146.2	330.3	211.7	270.0	97.4	42.0	116.6	0.817389198	1.275148767
917.4	1089.9	678.1	726.0	873.7	580.9	996.5	639.3	811.0	211.2	225.7	184.9	0.813864804	1.268575004
105.3	62.4	71.2	71.9	78.3	97.1	105.1	63.9	81.0	16.7	16.7	16.6	0.771305286	1.267730496
273.9	194.9	216.4	203.3	186.9	228.8	108.7	171.5	217.4	14.9	49.9	31.5	1.999693346	1.267591945
339.3	141.8	82.7	365.4	515.9	125.9	349.1	206.6	261.8	230.1	115.9	171.0	0.749980904	1.267344305
385.1	197.9	308.8	305.8	276.7	263.6	551.5	228.8	289.7	167.5	179.3	61.6	0.525242085	1.266063467
755.2	1181.4	595.6	1150.9	527.7	488.3	1361.3	619.4	783.2	568.0	289.3	310.5	0.57532016	1.26434091
83.2	115.6	74.4	112.6	102.0	72.9	238.9	74.3	93.5	101.4	17.7	19.1	0.391135108	1.258416375
1351.8	786.8	816.0	1114.4	819.9	900.9	1264.5	766.9	965.0	202.2	245.3	224.1	0.763145269	1.258203597
151.0	186.7	124.1	118.8	150.2	65.5	221.5	105.7	132.7	53.0	31.4	40.8	0.599280532	1.255122628
438.9	198.9	230.3	208.8	153.6	3229.3	365.4	595.5	743.3	104.3	236.7	1222.0	2.034097751	1.248110958
304.4	427.2	210.3	293.5	234.0	168.9	531.2	219.0	273.1	170.7	83.9	91.1	0.514024849	1.246917527
288.6	349.8	158.5	220.6	191.6	139.0	280.0	180.5	224.7	53.7	75.2	80.7	0.802440476	1.244645099
299.8	240.8	186.8	318.2	199.6	376.2	381.2	217.6	270.2	129.1	43.7	73.8	0.708938909	1.241881127
1210.4	424.4	338.3	3804.0	1025.0	891.5	1622.9	1033.2	1282.3	1223.1	516.3	1281.4	0.790098506	1.241063363
456.4	392.6	338.5	423.5	377.1	308.8	467.8	308.8	382.8	55.2	127.6	54.1	0.818404025	1.239610992
290.4	301.3	196.7	224.8	201.3	260.2	402.0	198.4	245.8	95.6	88.7	45.0	0.61137091	1.239077099
1089.7	811.0	926.2	957.1	889.6	704.7	1097.0	724.9	896.4	292.0	180.7	131.2	0.817122455	1.236629602
160.0	425.5	385.9	19.6	44.6	82.6	80.3	151.4	186.4	35.7	73.4	176.8	2.320880033	1.231280832
75.4	71.7	46.3	70.3	52.1	50.7	114.1	49.6	61.1	33.4	20.1	12.7	0.535442964	1.230526457
59.2	93.2	55.8	126.1	44.9	80.9	141.6	62.3	76.7	86.1	26.6	29.9	0.541548964	1.230477107
464.4	350.3	356.0	443.3	441.3	208.0	482.0	306.7	377.2	91.9	73.4	95.8	0.78257472	1.229920661
430.7	577.7	347.2	367.3	334.9	403.4	531.7	333.8	410.2	163.7	37.1	89.4	0.771487681	1.228805943
66.0	81.4	36.6	231.9	301.6	71.7	186.1	107.1	131.5	108.0	69.0	108.1	0.706788465	1.228365085
885.0	680.1	486.4	465.4	330.2	1052.0	353.3	530.9	649.9	143.5	222.4	276.0	1.839163412	1.224053494
85.0	81.0	75.9	104.5	71.7	68.3	108.8	66.3	81.1	35.4	14.9	13.0	0.745372073	1.223463125
752.9	99.3	194.1	651.0	232.5	122.1	711.5	280.8	342.0	367.1	53.7	284.8	0.480664718	1.217889364
2322.5	2136.2	1482.2	1512.7	1397.7	1484.1	2154.7	1415.2	1722.6	268.0	284.2	398.8	0.799453592	1.217206763
224.0	146.1	148.2	125.4	121.1	346.8	87.3	153.1	185.3	24.0	74.3	87.4	2.122670333	1.21010233
304.1	353.1	208.9	260.3	163.3	143.2	371.0	197.6	238.8	99.3	65.6	81.9	0.643641297	1.208464056
197.1	196.1	199.3	172.4	143.4	211.8	274.5	154.9	186.7	94.9	31.0	24.8	0.680035456	1.20534177

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.17316.1.S1_at, CK461627, C1QC	2024.8	1830.9	1393.1	3971.1	5414.0	1256.3	855.8	1768.1	709.7	966.3
Ssc.28336.1.A1_at, CN164481, SH3BP5	1104.0	897.4	921.8	770.6	1089.4	451.1	480.6	657.7	456.2	629.6
Ssc.8833.1.S1_at, NM_214390.1, IL15	79.1	174.9	63.2	86.1	131.0	28.6	85.0	55.8	39.8	71.9
Ssc.2117.1.S1_at, BF710130, HIC2	237.6	180.5	154.1	262.4	153.2	267.0	232.0	378.5	420.6	192.6
Ssc.29589.1.A1_at, CO941202, KLHL7	283.0	182.7	143.5	244.7	252.9	63.4	111.6	121.6	113.2	165.7
Ssc.20172.1.A1_at, BX676733, ANTXR1	2920.7	4813.8	3282.2	3911.2	4131.7	2799.5	2154.5	2317.7	1455.8	2458.9
Ssc.8998.1.A1_at, BI401371, PNRC1	65.1	81.8	55.3	63.2	111.1	56.6	61.4	47.9	25.9	49.5
Ssc.2642.1.S1_at, BX666077, TST	257.9	232.5	148.4	212.3	241.8	147.5	93.7	172.6	35.2	192.9
Ssc.17458.1.S1_at, CN153596, DMXL2	193.6	185.0	47.2	167.5	214.6	44.9	90.9	67.1	33.2	150.5
Ssc.5438.1.S2_at, NM_213982.1, CD47	501.1	683.3	538.8	1040.4	839.8	596.8	407.1	567.9	273.5	454.1
Ssc.20445.1.S1_at, BX675815, SMC2	161.1	90.9	71.3	85.3	127.5	61.4	72.4	56.1	28.3	61.7
Ssc.1414.1.A1_a_at, CN165038, NCOA1	551.3	524.2	476.2	639.9	576.1	291.6	347.5	401.5	184.5	437.7
Ssc.3941.2.S1_at, BP167918, MAPK9	286.8	381.7	281.0	185.8	300.7	532.4	672.2	270.2	411.9	302.9
Ssc.24342.2.A1_at, CF360236, SLIT2	56.5	46.2	41.1	67.9	63.6	15.6	33.1	29.4	14.7	57.9
Ssc.9198.1.S1_at, CK463204, AHCYL2	325.1	307.0	387.1	397.0	492.4	253.4	273.6	252.2	171.0	253.2
Ssc.24234.1.A1_at, CK452621, TNFAIP8	699.5	1065.6	688.2	537.9	876.3	333.3	542.5	213.8	246.1	394.0
Ssc.28042.1.A1_at, CN031729, GRIP1	204.7	342.0	95.6	490.5	482.9	89.0	59.1	228.5	119.1	119.0
Ssc.12715.1.S1_s_at, CN164024, C1orf21	292.0	230.6	302.6	191.9	313.2	214.5	181.9	134.8	101.5	229.0
Ssc.5322.1.S1_at, CF179629, C1orf174	323.5	355.4	295.9	373.2	386.2	200.7	142.5	248.1	97.0	255.1
Ssc.10593.1.S1_at, CB288192, IFI44L	192.4	240.2	156.3	110.2	298.3	88.1	103.4	87.4	60.5	129.7
Ssc.30967.1.A1_at, CO956825, CRISPLD2	1001.8	1344.9	1904.8	1777.8	1407.9	1323.5	883.2	1157.1	380.4	965.6
Ssc.6931.1.A1_at, BF703328, HSPA13	1250.1	1153.6	1110.5	760.3	902.8	2097.6	1791.4	1184.7	2080.4	1506.8
Ssc.4863.1.S1_at, BI405218, CTNNAL1	2781.2	4098.6	2362.0	4281.8	3543.8	1495.0	1144.1	1799.2	993.9	1889.4
Ssc.13442.1.S1_at, AJ659028, PIK3C2A	1487.2	2249.9	842.8	2759.9	3097.6	1354.1	1201.1	1685.5	1012.6	1701.1
Ssc.17030.1.S1_at, CK466018, MCM7	916.5	776.2	741.2	1021.1	1041.5	466.8	639.6	649.0	524.0	510.7
Ssc.6093.1.S1_at, BF710870, MAP1B	426.7	217.6	532.1	506.7	453.7	665.7	639.4	1071.4	335.5	728.4
Ssc.1600.1.A1_at, CK457588	234.1	256.9	124.5	136.8	157.5	273.5	48.2	47.4	50.4	83.0
Ssc.2814.1.S1_at, BQ604514, PBXIP1	1298.1	1010.9	982.1	1583.2	1570.3	878.1	504.1	1169.3	336.9	945.0
Ssc.7297.1.S1_at, NM_001001864.1, MAOB	323.6	586.2	236.3	507.7	520.3	273.1	86.5	346.4	214.3	436.5
Ssc.27572.1.S1_at, CN161469, MCCC2	397.7	519.8	300.9	343.7	587.2	303.0	309.5	340.5	180.5	203.8
Ssc.18473.1.A1_at, CF368421, ARRB2	502.7	361.4	333.0	706.7	782.5	308.8	285.7	405.8	319.2	356.6
Ssc.13846.1.A1_at, CB472907, LAPTM4B	1447.9	1284.9	1665.7	1911.2	1585.8	926.4	969.2	1298.4	688.4	1190.5
Ssc.5995.1.A1_at, BF444726, CRISPLD1	186.9	475.0	379.1	1351.6	778.8	271.0	252.7	533.3	67.0	165.7
Ssc.26147.1.S1_at, BX921211, LASS3	1419.4	1297.2	1047.1	1307.1	1402.5	693.1	693.2	984.2	513.6	1000.4
Ssc.20101.1.S1_at, BX676643, IFI6	1087.8	1552.0	2012.8	2236.5	3599.0	1128.5	876.2	2166.5	790.6	1802.7
Ssc.28329.2.S1_a_at, BP434478, POLB	354.9	567.4	623.3	72.2	288.7	1095.7	500.4	145.5	760.7	377.9
Ssc.26815.1.A1_at, CN160502, PRSS35	90.3	153.8	105.4	64.6	108.5	392.3	180.5	64.3	150.7	114.9
Ssc.7957.1.A1_at, CN165035, EIF3H	740.6	568.8	866.3	336.8	370.4	842.6	1302.8	1019.6	1273.5	711.9
Ssc.30653.1.A1_at, CO937483, KIFAP3	56.9	49.4	49.0	39.0	41.1	38.4	16.6	33.5	32.4	31.3
Ssc.3355.1.S1_at, BI400302, HDAC1	1485.2	1317.2	1549.8	1727.1	1478.3	1049.1	972.0	1065.4	872.4	1069.6
Ssc.7218.1.A1_at, BQ599611, KIAA0101	93.4	44.0	38.0	145.1	103.4	29.7	33.7	67.8	24.4	57.3
Ssc.15867.1.S1_at, AY010066.2, KPNA1	113.1	134.4	139.0	44.0	138.7	249.2	215.1	107.7	211.8	113.0
Ssc.22072.2.S1_at, CF790268, TSPAN2	2173.4	3531.9	1211.4	2928.6	4584.5	1246.8	1108.4	1511.2	924.8	2907.8
Ssc.15736.2.A1_at, CN160894, TTC3	731.5	781.1	632.1	598.5	808.8	533.7	461.1	505.4	364.4	493.2
Ssc.6363.1.A1_at, CN160110, DAAM1	1705.0	1405.3	1697.0	1923.7	1569.2	1434.8	830.7	1154.4	832.7	1082.9
Ssc.14386.1.A1_at, CN162732, CCNG2	456.5	413.7	285.3	724.2	539.0	233.1	181.8	240.8	94.1	212.4
Ssc.1959.1.S1_at, BF710621, LAMA2	1362.2	1121.1	1107.3	1710.2	552.1	1088.0	743.5	814.3	437.3	703.9
Ssc.4434.1.S1_at, BX922497, CALML4	1106.4	1220.9	879.0	721.1	1056.3	99.4	301.1	713.9	287.9	304.0
Ssc.1314.1.S1_at, CO992000, WDR19	373.3	714.0	595.0	1275.5	888.3	421.8	409.6	328.5	139.6	485.5
Ssc.25591.1.S1_at, BX919044, ZCCHC11	418.7	200.2	232.3	146.3	254.9	149.6	179.5	234.9	123.8	143.9
Ssc.23233.1.S1_a_at, CN163548, SLC25A33	218.3	101.6	248.9	138.1	240.2	307.3	318.3	287.4	397.2	209.6
Ssc.1376.1.S1_at, CN162210, PHTF2	1585.9	2096.6	1306.2	2696.1	1694.7	888.4	1071.1	1481.0	597.4	1370.6
Ssc.22072.1.A1_at, CF790600, TSPAN2	269.7	393.0	116.2	322.8	412.7	96.4	100.3	157.1	77.9	314.5
Ssc.9707.1.A1_at, BX666261, BTG2	1480.6	2068.1	1488.8	1658.8	1739.9	1422.5	711.2	1776.8	701.5	936.7
Ssc.9245.1.S1_at, NM_214406.1, GALM	588.5	515.2	391.0	678.7	881.4	557.2	338.1	355.7	146.2	436.7
Ssc.1799.1.S1_at, CK451764	683.0	907.9	577.5	935.0	812.0	347.5	204.9	326.9	118.2	357.8
Ssc.9586.2.S1_at, CF791763, SDPR	1623.0	2768.6	1023.2	1134.5	2616.5	1130.7	993.7	1057.2	1325.0	1383.7
Ssc.3809.1.A1_at, CK466108, MUM1	735.2	824.1	631.2	866.3	940.2	502.3	431.5	627.8	319.1	728.7
Ssc.8819.1.A1_at, CF364996, HPS3	634.8	750.4	483.7	1205.2	1012.8	341.3	443.2	688.7	237.6	577.1
Ssc.17250.1.S1_a_at, BM189976, QDPR	1579.5	1512.3	1224.6	2502.5	1832.3	987.7	655.1	784.4	491.4	656.4
Ssc.2158.1.A1_at, CF792703, MLLT3	756.5	981.4	607.3	1711.2	1396.4	489.4	524.7	728.0	204.2	806.4

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
1887.4	190.6	516.8	3993.7	868.7	577.0	2926.8	1111.2	1339.0	1706.1	418.3	1424.4	0.457510757	1.204990221
851.6	673.5	607.2	682.2	612.5	433.4	956.6	535.0	643.4	140.2	100.3	135.7	0.672562301	1.202526914
55.4	52.5	39.9	104.2	41.6	111.9	106.9	56.2	67.6	45.6	22.9	32.0	0.632447439	1.202122614
482.0	277.4	398.9	249.6	331.0	406.3	197.6	298.1	357.5	49.9	97.4	87.6	1.809745563	1.199212898
142.3	127.5	173.6	188.6	126.8	68.6	221.4	115.1	137.9	56.8	36.4	42.2	0.622967112	1.198088619
2656.8	3386.2	1988.5	2187.8	4036.9	1813.8	3811.9	2237.3	2678.3	740.1	497.3	873.1	0.702620552	1.197138192
26.3	47.8	38.2	52.9	96.5	84.9	75.3	48.3	57.8	22.2	13.6	27.3	0.767153608	1.196988534
162.6	169.6	157.5	125.0	191.9	113.5	218.6	128.4	153.4	42.6	64.0	29.1	0.701573794	1.194500701
73.1	199.6	58.5	62.6	72.0	87.3	161.6	77.3	92.2	66.1	46.5	53.6	0.570512027	1.192231419
569.3	711.6	530.2	576.5	438.1	457.0	720.7	459.9	547.1	223.1	130.4	98.7	0.759167268	1.189694413
72.2	78.9	62.4	76.9	52.6	56.4	107.2	56.0	66.6	36.6	16.6	11.0	0.620841883	1.18911516
478.5	479.4	332.0	457.6	376.5	244.0	553.5	332.6	394.7	60.9	99.5	95.0	0.712986716	1.186753268
668.5	553.3	503.0	388.2	513.5	490.8	287.2	437.9	519.6	69.7	166.5	91.3	1.809018106	1.186403909
42.0	25.1	40.9	26.7	57.6	22.2	55.1	30.1	35.8	11.3	17.5	13.6	0.649291682	1.186131387
287.9	288.0	251.7	288.0	222.0	372.7	381.7	240.7	285.1	73.0	40.0	50.6	0.746751546	1.184352667
447.4	459.0	341.8	425.8	341.4	435.2	773.5	345.9	408.4	202.6	130.9	53.0	0.528032752	1.180647897
178.8	197.0	138.6	185.1	97.4	73.4	323.1	122.9	145.1	173.0	64.0	50.8	0.448876648	1.179843826
200.7	160.7	143.4	190.2	270.2	252.6	266.1	172.3	203.0	52.4	53.6	50.0	0.762860508	1.177710727
184.7	242.8	222.1	214.4	233.3	226.6	346.8	188.7	220.7	36.9	68.2	20.1	0.636172298	1.169440322
120.4	123.6	88.9	139.0	70.3	114.3	199.5	93.8	109.4	73.0	25.3	25.2	0.548509458	1.166240318
741.6	566.3	1404.8	753.3	2119.3	997.0	1487.4	942.0	1097.1	360.9	357.5	579.0	0.737542355	1.164646057
2732.6	2243.9	2025.5	1183.0	1651.1	2258.5	1035.5	1732.2	2015.8	199.4	390.1	538.8	1.946735428	1.163716627
1826.0	2317.1	1305.1	2526.1	1254.8	990.3	3413.5	1464.3	1703.2	828.5	392.9	622.4	0.4989727	1.163156505
1810.9	2098.8	1214.6	1598.2	1278.1	1703.3	2087.5	1390.9	1617.3	923.1	301.5	333.0	0.774769898	1.162801008
830.5	814.2	573.1	626.6	746.4	288.1	899.3	558.0	646.5	137.4	81.6	203.1	0.718873939	1.158530758
1040.4	627.5	649.7	392.5	1426.9	639.6	427.4	688.1	796.1	124.5	262.6	372.8	1.862832273	1.15698756
90.7	138.3	112.4	118.6	112.0	125.2	182.0	100.5	116.2	59.7	97.9	15.9	0.638601891	1.156218905
840.1	1032.1	804.2	1056.7	939.9	641.6	1288.9	766.7	885.8	290.4	339.1	156.2	0.687216171	1.155327733
325.1	503.1	344.7	363.5	118.6	224.0	434.8	271.4	313.2	147.7	132.6	130.8	0.720221394	1.154063483
320.9	446.2	248.4	327.5	259.8	245.9	429.9	267.5	308.1	120.3	70.7	76.7	0.716783759	1.152010269
521.6	352.9	397.8	363.7	344.1	333.8	537.3	335.2	385.7	201.7	47.0	70.1	0.717808882	1.150438518
1275.2	1204.5	1095.6	1125.1	1076.5	1195.3	1579.1	1014.6	1162.0	235.4	238.6	75.9	0.735883309	1.145334358
239.0	352.9	171.1	218.6	634.3	155.3	634.3	257.9	295.2	454.4	173.9	180.2	0.465409598	1.144452198
1043.2	931.3	972.8	874.0	783.2	725.4	1294.7	776.9	888.3	148.9	209.9	119.0	0.686138961	1.143411851
1775.4	1064.5	2697.3	1254.7	1010.0	1445.6	2097.6	1352.9	1541.3	948.4	603.7	631.2	0.734761301	1.139219455
968.1	306.0	709.4	414.3	417.5	1080.2	381.3	576.0	649.3	222.5	365.5	321.8	1.702727511	1.127091869
248.9	205.9	196.1	50.5	274.3	238.1	104.5	180.5	202.3	32.6	126.0	79.7	1.935514734	1.120527307
1735.3	717.5	1754.0	288.8	903.4	1521.0	576.6	1030.1	1153.3	229.6	259.9	605.7	2.000300623	1.119654137
33.7	52.5	25.6	31.6	30.0	30.7	47.1	30.4	34.0	7.2	8.2	9.4	0.722529029	1.117498905
1291.6	1070.2	1089.7	969.7	758.2	1540.9	1511.5	1005.7	1120.1	147.9	84.3	269.6	0.74100905	1.113701899
47.7	33.3	52.1	40.4	77.6	33.3	84.8	42.6	47.4	44.5	18.9	16.6	0.559094126	1.113198685
348.8	133.5	184.5	124.6	173.6	230.6	113.8	179.4	199.3	40.5	64.7	82.6	1.750409932	1.110987214
1991.4	2302.0	1446.5	2109.6	995.9	1379.2	2886.0	1539.8	1704.1	1286.1	794.1	505.6	0.590479425	1.106702169
627.5	568.8	476.3	488.5	532.9	434.4	710.4	471.6	521.4	91.9	65.3	69.7	0.733952703	1.105691747
1367.5	1108.8	981.1	940.6	1377.6	1226.9	1660.0	1067.1	1167.1	191.1	251.9	188.3	0.703045308	1.093696311
237.0	176.8	185.9	217.7	266.2	179.1	483.7	192.4	210.5	162.7	59.5	36.3	0.435047753	1.093587612
921.4	833.6	967.4	488.2	905.0	847.5	1170.6	757.4	827.2	423.3	233.5	173.2	0.706644	1.092135375
487.5	507.1	235.7	564.9	219.2	219.6	996.7	341.3	372.3	197.3	225.4	163.7	0.37355111	1.091054719
423.2	544.8	335.0	367.0	313.6	352.4	769.2	357.0	389.3	339.4	133.7	84.7	0.506140419	1.090569561
201.5	175.2	167.2	203.2	190.0	151.1	250.5	166.3	181.4	102.5	43.2	20.5	0.72407644	1.090337061
298.6	153.4	420.3	214.5	329.2	560.3	189.4	304.0	329.4	65.8	67.2	146.1	1.738904727	1.083640391
1614.2	1259.6	1042.5	1160.5	1025.0	927.4	1875.9	1081.7	1171.5	539.2	358.8	245.6	0.624518009	1.083048288
184.8	310.8	113.8	166.8	109.6	82.1	302.9	149.2	161.3	118.9	97.0	82.6	0.532609174	1.080921111
1016.9	971.3	1315.4	806.8	890.8	2190.8	1687.2	1109.7	1198.7	240.2	473.9	516.0	0.710430447	1.080132884
375.1	541.1	282.0	446.5	401.6	329.8	611.0	366.8	396.0	184.2	150.6	91.1	0.648187552	1.079711725
241.9	392.3	184.8	597.8	255.9	78.9	783.1	271.1	291.9	151.5	105.2	181.3	0.372801417	1.077006321
1822.2	1688.6	1416.4	1254.3	609.1	801.4	1833.2	1178.1	1265.3	818.1	169.4	481.3	0.690247078	1.074082248
581.8	669.2	435.3	703.8	563.9	405.5	799.4	521.9	559.9	119.7	161.0	120.4	0.700421149	1.072883932
560.7	501.4	403.9	577.8	522.5	373.4	817.4	457.6	490.0	290.6	180.2	83.5	0.599415205	1.070741728
931.3	805.3	781.3	622.1	597.5	842.8	1730.2	715.0	763.4	482.9	184.5	129.7	0.441200835	1.067668998
603.2	875.2	420.3	775.4	414.3	431.9	1090.6	550.5	586.7	457.1	235.2	200.2	0.53799577	1.065711241

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.8925.1.S1_at, CF366016, HBA2	3445.1	1274.6	1499.9	2797.9	4105.0	4380.1	1419.1	4488.9	2815.3	11403.4
Ssc.22157.1.A1_at, CF788191, PHLPP	113.4	89.2	108.3	103.3	91.9	60.3	89.9	73.8	46.2	61.8
Ssc.7936.1.S1_at, BX673388, INCENP	180.1	227.8	205.4	184.9	240.1	215.9	129.2	91.5	48.7	163.1
Ssc.670.1.S1_at, NM_214392.1, LYZ	4733.2	6847.2	4626.4	5972.2	9513.8	1259.6	537.7	4094.0	2573.5	2908.6
Ssc.24221.2.A1_at, BI181166, NDUFS4	1194.1	1189.9	949.1	2438.1	1784.4	683.9	700.9	1031.1	191.1	967.4
Ssc.11528.1.A1_at, BI186168, VWA5A	203.5	299.0	239.0	380.5	360.5	161.2	139.1	208.6	89.1	203.3
Ssc.11025.1.S1_at, CO955623	1511.1	1923.5	1013.1	2763.9	2420.8	726.8	500.4	1494.2	732.9	1678.0
Ssc.4303.2.S1_at, BG833879, EEF1E1	294.4	369.6	338.9	159.6	203.5	436.0	646.9	217.1	730.8	408.2
Ssc.29092.1.A1_at, BI398847, KRAS	109.8	136.0	134.0	67.8	67.9	234.1	146.8	110.5	204.1	148.3
Ssc.6972.1.A1_at, BF704050, HSPA13	488.5	391.0	530.4	457.0	373.3	914.9	619.2	641.9	824.8	506.1
Ssc.8125.1.A1_at, BF712776, CBX6	1281.6	2094.1	1011.2	2145.0	1812.5	965.1	818.6	1304.2	742.8	1369.7
Ssc.17507.1.S1_at, CO955813, TNRC6C	1066.2	838.7	614.4	948.4	1337.6	405.0	550.2	713.0	321.2	939.4
Ssc.5901.1.A1_at, CF180142, NADSYN1	228.3	175.3	175.0	142.1	335.9	99.5	183.9	143.7	111.1	132.0
Ssc.19354.2.S1_at, BX670759, CHCHD4	51.7	59.6	82.2	32.0	66.4	120.8	107.7	45.3	182.2	61.4
Ssc.8444.1.S1_at, CN160479, KIAA1109	648.0	701.4	487.2	962.0	814.7	481.7	348.8	407.4	215.8	662.8
Ssc.15296.1.S1_at, CA780867, CD53	653.3	818.1	785.4	1898.0	2209.9	691.3	570.9	1257.5	505.5	624.6
Ssc.3122.1.S1_at, CK454137, LAMA1	252.4	346.1	240.5	161.9	289.3	182.3	97.5	158.4	164.2	141.1
Ssc.5569.1.S1_at, BF190468, THRA	684.5	628.1	551.2	1078.9	941.0	399.0	290.9	517.9	218.3	637.6
Ssc.3914.1.S1_at, CK455943, C2orf7	447.5	419.2	423.4	494.9	650.1	315.4	289.5	260.1	227.4	321.6
Ssc.14164.1.A1_at, BQ600574	122.2	129.3	74.0	190.9	116.1	163.6	50.2	72.6	22.9	77.9
Ssc.21179.1.S1_at, AJ652061	288.0	134.4	269.5	193.3	181.2	336.8	314.5	275.2	453.7	255.1
Ssc.6685.1.S1_at, BP458282, CALU	489.3	673.9	552.3	355.8	515.2	876.1	858.7	502.7	1057.6	691.5
Ssc.21332.1.S1_at, BX672474, CDKL5	192.2	254.9	204.2	390.9	287.1	204.1	209.7	269.2	90.8	96.7
Ssc.13496.1.A1_at, CK459773, HISPPD2A	144.6	124.7	109.3	169.0	138.7	98.6	77.4	63.6	58.8	97.4
Ssc.17442.1.S1_at, CD572324, CCDC15	620.3	663.7	518.6	946.0	773.1	515.4	411.5	258.5	512.0	459.5
Ssc.2879.1.S1_at, BI403126, SLC25A25	215.6	225.2	224.6	103.2	279.3	346.5	362.9	285.3	356.3	266.1
Ssc.24543.1.S1_at, CK461525, AFF3	403.0	451.0	349.5	315.2	456.7	222.2	231.3	169.8	191.4	306.1
Ssc.1716.1.S1_at, CN165456, ASPN	1652.7	1708.3	2756.8	2411.8	1510.6	1773.1	1016.2	1028.5	957.5	1606.2
Ssc.3761.1.A1_at, CF360624, C6orf103	1361.6	1257.4	872.9	1943.1	2169.9	654.5	410.1	1113.1	868.0	790.6
Ssc.2168.1.S1_at, CK456510, KIAA1462	1196.2	969.8	1153.6	1081.1	813.9	1819.5	1652.4	1471.2	1881.4	1450.9
Ssc.12977.2.S1_at, CK449388, PDLIM4	246.0	175.2	252.0	65.9	121.5	402.7	260.1	134.1	309.6	325.4
Ssc.31010.1.S1_at, BF191571, CPNE2	392.0	351.8	347.1	400.4	385.0	238.8	274.7	244.3	193.6	267.4
Ssc.2709.1.S1_at, BQ602779, ERO1L	568.4	534.6	384.7	657.2	730.0	336.6	235.2	438.6	111.1	292.8
Ssc.7024.1.A1_at, CF368959	93.6	53.1	97.9	203.8	155.4	73.9	61.1	158.6	46.3	59.8
Ssc.27717.1.S1_at, BE013963, CDC2L6	143.7	132.6	142.9	235.5	151.6	110.9	78.4	80.6	30.3	113.4
Ssc.29024.1.S1_at, CO950263, MAN1A1	3012.3	4088.4	1885.6	5107.1	4514.8	1892.7	2806.9	2984.3	1901.9	2372.2
Ssc.10952.1.S1_at, AJ300958, DLG1	65.5	74.9	123.2	202.2	148.6	81.6	69.6	79.0	81.6	97.4
Ssc.26146.1.S1_at, BX914993, CXCL9	132.2	609.5	187.4	479.3	1206.4	268.7	179.5	432.5	497.4	210.9
Ssc.30990.1.A1_at, CO942981, HSPA14	808.4	790.1	866.9	443.9	492.4	887.7	1304.6	817.9	1687.9	824.1
Ssc.529.1.S1_at, CO950937, NPC2	2108.8	2416.7	2275.5	2239.8	4037.3	1932.7	1634.2	1719.5	1246.7	2007.1
Ssc.14205.1.S1_at, BQ600780, TPP2	194.5	206.4	171.9	115.4	149.9	263.7	293.7	185.3	353.9	224.5
Ssc.10789.1.A1_at, CK464666, TPRG1	417.2	384.3	378.4	401.2	764.7	329.2	214.7	246.6	120.4	455.0
Ssc.26463.1.S1_at, CN069680, KLF15	522.8	717.3	385.8	620.0	1203.4	333.0	393.7	273.4	198.6	255.4
Ssc.10548.1.A1_at, CF175781	898.6	1017.1	1171.8	509.6	429.9	1226.7	968.5	970.6	1296.4	1867.7
Ssc.19796.1.S1_at, BX675301, IGSF1	1300.3	2006.1	511.1	1295.5	1318.7	1222.9	307.4	1093.4	623.3	925.7
Ssc.3003.1.S1_at, CK454998, LRIG2	320.8	1003.3	481.9	657.3	862.9	175.2	430.0	332.1	315.5	461.6
Ssc.29353.1.A1_at, CO954247	141.4	212.6	93.5	183.6	130.2	75.0	76.4	105.3	39.2	106.0
Ssc.25023.1.S1_at, CK465919, NUF2	135.8	67.6	145.1	100.8	121.5	25.0	39.4	57.2	21.9	117.4
Ssc.21898.1.S1_at, CN153396, ERO1L	796.3	640.4	494.1	1526.9	919.9	403.3	267.6	574.9	127.4	434.5
Ssc.23077.1.A1_at, CK464852, APAF1	671.6	769.1	654.0	1287.3	1471.6	542.9	568.7	731.7	476.4	510.2
Ssc.2096.1.S1_at, CK457095, CLCN6	140.2	152.3	187.7	168.7	191.8	91.6	66.8	141.4	83.0	103.5
Ssc.8789.1.S1_at, BF711868, SRXN1	195.3	118.5	211.7	80.9	96.3	227.2	231.9	266.5	360.3	168.4
Ssc.22625.1.S1_at, BX666116, PEX3	430.3	736.6	390.3	501.5	913.0	367.1	349.3	281.0	220.0	478.2
Ssc.26270.1.S1_at, BX919779, FAM110B	106.8	183.4	55.1	183.1	139.1	77.4	49.3	70.2	34.0	64.5
Ssc.30371.1.A1_at, CO990887, CLSPN	18.7	23.3	29.9	25.7	30.4	59.2	13.9	36.7	22.0	60.4
Ssc.1536.1.A1_at, BF709823, PCDH7	329.0	326.7	361.0	172.7	255.3	339.9	146.3	210.5	85.8	129.8
Ssc.16620.1.A1_at, BF709392, ANKRD44	120.8	82.3	101.1	147.3	136.9	95.5	48.7	83.5	51.3	85.9
Ssc.1813.1.S1_at, BX925475, PRODH	233.6	208.1	164.9	232.1	249.0	65.2	83.4	153.5	72.6	120.0
Ssc.5677.1.A1_at, BF712001, ST8SIA4	468.3	637.9	255.9	964.2	1442.3	105.3	281.6	416.5	168.5	633.5
Ssc.23810.1.S1_at, CK453668, NFIA	233.8	373.3	288.1	190.2	499.6	294.5	141.3	156.3	128.4	318.5
Ssc.30613.1.A1_at, CO992640, ARL4A	266.6	180.3	98.2	245.0	210.0	80.9	48.9	82.3	28.8	101.7

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
5984.4	9246.5	10488.5	2856.0	1082.0	1662.2	2624.5	4901.4	5219.9	1222.9	3847.0	3998.1	1.988924875	1.064996926
99.7	79.2	61.9	81.8	55.2	45.9	101.2	66.4	70.6	10.4	16.4	19.8	0.697655272	1.063504016
136.1	172.0	110.2	141.6	120.4	146.8	207.7	129.7	137.9	26.2	64.4	21.6	0.663825484	1.063001234
1321.6	161.4	1592.7	5107.9	2048.2	4271.8	6338.6	2274.7	2417.3	1999.0	1400.8	1886.0	0.381358963	1.062684275
734.8	943.7	488.3	678.9	1403.5	302.3	1511.1	714.9	758.6	602.8	331.4	384.3	0.502000724	1.061133803
155.8	211.7	137.2	178.7	179.7	156.3	296.5	160.3	169.9	76.0	49.2	26.0	0.57301855	1.060152253
1267.0	1028.8	789.8	1505.1	494.0	1432.0	1926.5	1026.5	1086.1	698.6	523.4	392.3	0.563782996	1.058118842
793.8	468.2	393.9	295.9	360.5	781.4	273.2	487.8	515.6	89.2	204.1	217.9	1.887323084	1.057024737
211.1	152.1	142.4	146.6	152.5	264.9	103.1	168.8	178.3	33.8	49.5	49.4	1.729065632	1.056332464
998.0	829.5	692.7	412.6	704.9	805.5	448.0	701.4	740.5	65.8	165.3	194.7	1.652828616	1.055823282
1313.9	2065.8	813.0	1275.8	498.1	594.4	1668.9	1040.1	1093.5	502.7	283.5	584.7	0.655229855	1.051361434
857.7	748.7	551.1	558.2	621.7	339.5	961.1	585.8	612.8	268.4	247.6	178.9	0.637646626	1.046190704
150.6	163.2	146.7	93.7	190.1	95.5	211.3	134.0	140.0	76.2	32.8	38.3	0.662344627	1.044215657
173.8	73.4	95.0	64.2	60.7	180.4	58.4	103.5	107.9	18.5	54.0	54.9	1.848521183	1.04287463
475.0	642.1	288.4	611.0	316.6	310.4	722.7	423.3	440.6	178.3	165.6	158.9	0.609668908	1.040829987
1412.4	261.5	473.1	1147.8	690.1	546.4	1272.9	730.0	755.2	724.1	302.7	437.5	0.59328536	1.034600069
136.8	143.6	194.6	235.8	140.3	69.8	258.0	148.7	153.5	67.7	32.2	56.6	0.594804423	1.032167675
393.2	552.5	391.6	477.1	473.1	264.4	776.7	412.7	425.3	223.5	169.2	99.2	0.547566324	1.03047116
291.9	262.0	237.9	276.5	278.0	392.5	487.0	282.8	289.8	96.0	39.4	53.5	0.595047431	1.024752475
62.0	73.9	77.4	95.3	99.9	65.6	126.5	77.4	79.0	41.9	52.8	15.5	0.624637681	1.020359848
459.5	307.6	325.7	238.5	316.2	345.7	213.3	327.1	332.2	64.0	77.7	72.2	1.557576894	1.015715771
1012.8	484.5	860.1	503.7	590.0	1403.0	517.3	797.3	809.0	114.7	209.6	358.7	1.563921644	1.014669978
181.4	272.3	119.1	153.3	169.7	158.3	265.9	174.1	175.7	79.7	77.7	51.8	0.660811455	1.00909439
88.7	80.7	73.4	81.3	51.6	102.5	137.3	79.2	79.7	22.4	18.5	16.9	0.580649862	1.006821627
414.8	480.2	532.2	299.2	309.2	569.4	704.3	431.4	434.2	163.0	105.6	113.3	0.616416314	1.006459888
506.2	287.4	348.4	206.2	229.7	372.6	209.6	323.4	325.1	64.6	44.5	109.8	1.551118109	1.005142951
219.8	313.8	183.9	263.6	184.7	183.4	395.1	224.2	224.9	62.1	52.0	53.8	0.569167426	1.00315251
1317.5	1524.5	1153.1	848.9	2262.5	550.1	2008.0	1276.3	1276.1	544.8	382.9	593.5	0.635495309	0.999843297
931.0	530.9	600.5	1328.6	691.8	512.4	1521.0	767.3	765.9	527.8	260.1	315.0	0.503535002	0.998184014
2111.8	1533.7	1482.1	1294.2	1847.7	1605.1	1042.9	1655.1	1645.8	154.1	196.1	290.7	1.578037306	0.99437288
397.9	216.0	282.9	251.7	173.8	386.3	172.1	286.4	284.8	80.1	99.3	90.8	1.654465877	0.994366459
271.1	329.9	265.1	294.4	124.0	169.5	375.3	243.8	242.3	24.2	31.8	78.8	0.645774485	0.994147249
271.1	352.4	203.5	338.0	410.5	109.4	575.0	282.9	280.8	131.0	121.5	110.2	0.488393799	0.992776167
97.0	81.2	66.4	72.2	94.2	64.3	120.8	79.9	79.2	59.0	45.0	14.0	0.655984322	0.990951547
92.2	89.8	67.3	86.6	64.1	90.5	161.3	82.7	81.8	42.0	33.6	12.6	0.506945306	0.988273694
3516.6	3486.4	1728.3	1939.9	1495.8	1981.9	3721.6	2391.6	2358.2	1280.4	503.2	902.4	0.633631947	0.986013547
55.3	69.3	94.9	66.3	141.7	56.5	122.9	81.8	80.7	56.0	10.0	33.1	0.656467014	0.985663082
654.8	153.5	130.7	589.3	122.8	225.6	523.0	317.8	312.8	430.6	140.0	243.2	0.598101831	0.984214391
1596.9	938.7	1140.8	772.4	872.8	1197.8	680.3	1104.4	1086.6	196.5	383.5	297.3	1.59709361	0.983816836
2160.2	1627.9	1592.9	1703.4	1225.8	1747.9	2615.6	1708.0	1676.4	802.3	299.3	300.8	0.640899672	0.98144657
307.9	297.4	263.6	192.1	196.9	293.6	167.6	264.2	258.6	36.4	64.6	51.8	1.542675894	0.978666768
234.8	355.7	257.0	318.8	219.9	213.3	469.2	273.2	266.6	165.9	126.2	57.9	0.568214113	0.975852307
276.5	321.1	242.4	409.9	295.5	147.6	689.9	290.8	282.2	312.1	74.9	86.9	0.409020188	0.970245054
1229.0	1563.2	1222.4	764.1	1823.7	766.4	805.4	1266.0	1228.1	322.6	367.5	423.2	1.524873769	0.970104846
983.4	1048.2	938.6	917.9	608.2	359.7	1286.3	834.5	809.3	529.2	370.4	267.8	0.629175283	0.969795736
425.1	377.5	259.3	392.8	148.8	388.2	665.2	342.9	332.0	276.4	112.5	106.2	0.498992845	0.968122958
71.1	114.2	63.7	106.7	64.1	47.0	152.3	80.4	77.8	46.6	27.5	26.6	0.510968081	0.967902463
43.3	43.3	36.9	53.1	55.4	70.9	114.2	52.2	50.5	30.9	39.0	12.1	0.442215604	0.967484349
268.0	533.9	253.7	391.1	542.4	108.0	875.5	361.5	349.5	397.9	170.5	171.5	0.399210374	0.966744113
676.3	600.1	439.3	592.2	509.7	448.5	970.7	566.0	544.4	381.3	98.9	94.1	0.560769326	0.961783102
88.5	105.8	146.2	89.5	79.1	51.3	168.1	97.3	93.4	22.2	28.1	31.5	0.555489473	0.960312564
358.9	91.1	295.0	82.2	198.8	418.5	140.5	250.9	240.8	59.3	70.6	139.9	1.713035435	0.959698637
264.3	433.5	233.7	457.1	196.4	362.6	594.3	339.1	324.6	223.0	97.2	108.8	0.546152034	0.957183298
48.9	67.7	62.0	43.7	65.5	51.5	133.5	59.1	56.6	54.4	17.4	9.8	0.423595506	0.95717671
34.8	32.8	34.2	28.0	76.5	13.7	25.6	38.4	36.7	4.9	21.1	21.0	1.432291667	0.953867499
212.7	198.7	196.7	107.6	125.4	201.9	288.9	182.5	173.8	75.6	98.7	45.1	0.601624328	0.952720231
84.8	92.2	50.3	66.5	69.4	53.4	117.7	73.0	69.4	26.4	21.5	16.7	0.590018128	0.951402211
110.6	124.8	104.2	101.8	60.2	63.1	217.5	98.9	94.1	32.9	37.1	26.4	0.43264074	0.951249916
356.2	524.2	255.2	321.7	140.7	227.8	753.7	321.1	304.3	464.0	211.0	131.4	0.403730828	0.947738881
248.1	333.8	147.7	191.1	168.0	92.6	317.0	207.8	196.9	122.8	91.0	84.3	0.62108307	0.947465512
65.8	96.4	52.1	77.5	22.4	75.3	200.0	68.5	64.9	65.8	29.2	25.4	0.324550878	0.947411948

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.15296.3.S1_at, CB480766, CD53	129.3	72.4	61.3	246.3	268.4	60.2	64.9	193.2	102.4	64.6
Ssc.20489.1.S1_s_at, CN166538, MDK	1490.6	1190.3	1113.9	3140.9	2378.1	1037.7	783.0	1634.7	1065.6	1472.7
Ssc.23897.1.S1_a_at, CK451782	491.6	803.4	460.4	944.9	786.9	451.9	349.4	478.7	257.9	570.3
Ssc.15824.1.S1_at, BG382957, KPNA2	144.9	236.1	266.2	108.3	183.8	262.3	576.2	192.5	485.9	270.3
Ssc.31070.1.S1_at, CO994289, GLG1	3276.5	2942.0	2768.2	2608.9	3038.3	1971.3	1573.3	2528.9	1371.4	1745.5
Ssc.6145.1.A1_at, CF368396, CYBRD1	1090.5	2058.7	896.6	1636.5	1573.6	1459.3	731.7	913.1	616.4	1029.4
Ssc.10085.1.A1_at, BI399794, SCP2	271.0	224.2	356.2	121.7	181.0	384.6	534.4	241.2	487.3	224.2
Ssc.6559.1.S1_at, BI182546, RPA2	349.2	318.9	375.3	586.5	687.6	429.4	238.6	297.3	161.6	390.0
Ssc.8808.1.A1_at, CO986712, PTPLAD2	41.6	28.2	23.0	34.0	66.1	22.2	19.7	39.7	27.2	19.0
Ssc.5382.1.A1_a_at, CO954481, TRIM35	63.0	68.0	58.4	117.2	84.5	56.9	36.4	48.9	58.6	50.9
Ssc.2035.1.S1_at, BF703604, ZNF530	221.4	408.5	169.4	458.8	386.6	189.9	117.7	218.3	170.7	358.3
Ssc.27871.1.S1_at, AW483183, ACSS2	344.2	377.9	299.2	476.9	583.8	243.2	179.0	359.4	96.6	263.3
Ssc.9586.1.S1_at, CO992707, SDPR	2845.8	4077.2	1956.4	2156.0	4243.7	2132.5	2034.7	1580.0	1791.1	2185.6
Ssc.13450.2.S1_at, CF179357, ERMN	142.6	175.9	162.1	231.1	267.0	118.9	91.9	111.7	95.0	153.8
Ssc.1294.1.S1_at, CF359694, NIT1	195.6	178.5	173.9	326.5	332.5	198.0	163.3	174.6	80.0	173.4
Ssc.26009.1.S1_at, BX926326, HLCS	117.1	241.4	93.8	218.8	210.3	56.3	41.5	104.7	85.3	110.0
Ssc.658.1.S1_at, NM_213867.1, IL8	47.9	99.5	86.7	227.8	202.1	256.1	161.4	826.3	413.9	256.0
Ssc.7864.1.A1_at, CN069777, IL1RAP	551.4	672.1	419.7	601.0	896.6	266.3	412.1	483.6	268.7	453.5
Ssc.3578.1.S1_at, BQ601162, MCOLN1	268.7	276.4	240.3	260.0	366.4	150.8	173.5	173.5	140.5	231.5
Ssc.11074.1.S1_at, U29948.1, CFD	741.4	1190.2	583.8	814.3	1552.8	714.0	417.6	631.3	456.8	417.4
Ssc.29750.1.A1_at, CO993759, TP53INP1	920.2	715.2	486.8	1220.5	1251.3	514.7	307.3	458.9	229.1	407.9
Ssc.15379.1.S1_at, CF362412, DGAT2	163.2	67.6	138.7	109.1	114.1	84.9	83.2	69.5	33.6	79.6
Ssc.17955.1.A1_at, CF175506, AZIN1	248.2	331.7	263.5	266.6	285.2	476.3	552.6	258.7	519.0	316.1
Ssc.14352.1.S1_at, AJ656944, RYR2	350.4	255.0	261.2	600.8	1036.8	295.1	136.6	178.6	120.0	249.6
Ssc.10047.1.A1_at, CN158718, BRI3P1	644.6	549.2	631.2	703.3	736.5	389.1	368.2	487.7	237.7	397.0
Ssc.30882.2.S1_at, CF795525, C1orf58	445.5	377.0	317.9	295.3	508.4	261.4	249.4	233.8	224.9	266.4
Ssc.19535.1.A1_at, CF362278, EFHC2	486.5	441.9	521.5	623.0	624.3	375.6	372.2	509.3	174.3	357.0
Ssc.8988.1.A1_at, BF708970, DSE	67.4	38.7	21.2	33.7	35.0	17.0	30.7	22.1	22.7	31.9
Ssc.3915.1.A1_at, CK464618, WEE1	693.1	652.1	722.7	447.8	610.8	939.4	1255.2	735.2	1871.7	882.9
Ssc.30072.1.A1_at, CO949532, GRK5	385.7	338.0	557.2	195.8	187.7	676.5	514.0	612.8	491.6	481.0
Ssc.10575.1.A1_at, BQ602804, TMEM59	2076.8	2366.4	2506.5	3927.5	2856.1	2093.4	1113.2	2469.5	1411.2	1994.5
Ssc.22470.1.S1_at, BX667242, PER3	541.0	446.2	406.7	506.7	625.6	206.6	377.7	420.6	187.6	335.7
Ssc.30628.1.S1_at, CO991625, PECR	35.0	33.6	24.2	55.1	32.0	25.8	29.8	15.9	25.0	14.5
Ssc.5595.1.S1_a_at, CK454919, TCF19	97.9	73.3	114.3	123.8	138.3	84.8	58.5	78.4	52.2	87.0
Ssc.26651.1.S1_at, CN154029, CYP39A1	125.6	206.3	147.8	280.9	236.3	128.4	131.3	192.9	74.6	126.7
Ssc.7944.1.A1_at, BQ599841, BAMBI	474.8	449.4	664.4	894.3	396.4	436.7	300.5	508.6	148.2	357.8
Ssc.3472.1.S1_at, CF792015	152.1	84.0	100.9	151.2	107.1	46.2	109.8	85.6	57.0	57.9
Ssc.18577.1.S1_at, BF442135, DYRK3	213.0	254.5	214.3	159.5	259.7	326.5	456.1	323.7	333.3	284.8
Ssc.1027.1.S1_at, BX672675, ASAH1	1152.1	1576.0	1076.0	1542.8	2204.4	641.3	701.2	1060.6	613.8	1094.4
Ssc.13732.1.A1_at, BQ603325	105.5	136.0	76.8	148.0	114.1	106.7	48.1	56.5	66.3	106.3
Ssc.10254.2.A1_a_at, CK462338, ZMYND19	502.4	624.9	569.3	271.8	419.6	687.6	903.3	426.8	1066.6	607.0
Ssc.24956.3.A1_a_at, CK462298, LSM12	260.9	239.1	243.9	206.6	189.7	327.0	444.9	315.8	413.4	325.1
Ssc.18247.1.A1_at, CN161639, IFT172	328.9	264.0	187.8	283.8	434.5	213.7	143.1	180.2	106.2	278.8
Ssc.9608.1.S1_at, BX666117, ZDHHC7	265.4	221.7	162.6	180.6	181.2	93.3	118.0	134.6	113.9	187.8
Ssc.15621.1.A1_at, BG894549, PCYOX1	3672.5	3997.4	3568.8	5147.8	4826.0	2438.3	2825.6	3293.3	2128.1	3441.3
Ssc.30752.1.S1_at, BX921277, IFIT1	282.3	481.4	377.3	447.0	536.9	285.3	167.0	245.3	174.0	339.1
Ssc.6528.1.S1_at, CK457991, AGPAT2	184.0	207.9	252.7	101.7	139.4	389.6	309.8	257.9	350.9	262.4
Ssc.21563.1.A1_at, CF788967, RASGEF1C	122.0	17.4	13.7	57.3	50.4	31.9	27.1	29.8	22.4	46.4
Ssc.28763.1.A1_at, CO951495	139.1	53.1	108.2	44.1	51.4	70.1	164.9	123.4	169.7	150.9
Ssc.8330.1.S1_at, NM_214356.1, RGS5	1933.4	1313.3	4358.3	1996.9	2485.6	8141.3	2789.6	2109.9	1039.1	4700.8
Ssc.16561.1.S1_at, CA779610, TRDN	730.0	539.5	561.2	934.2	821.5	463.4	384.8	461.3	268.3	624.5
Ssc.21723.1.S1_at, BX919975, RBMS2P	454.6	325.9	329.6	457.9	450.2	322.0	278.3	255.3	188.7	263.5
Ssc.19823.2.S1_at, BP157498, ABLIM1	290.7	347.8	228.0	88.1	468.4	163.9	222.4	108.8	174.6	249.8
Ssc.16444.1.S1_at, BQ602525, PTPRK	668.7	869.9	613.8	1765.9	1012.6	449.0	539.8	709.9	393.7	389.3
Ssc.9611.1.A1_at, BF711044, SESN1	1572.1	2086.3	1461.2	3382.2	2520.7	1947.0	568.2	1477.5	489.5	1625.1
Ssc.5296.1.A1_at, BI344188, PIK3AP1	189.8	217.9	116.4	281.5	407.5	163.9	103.6	176.1	98.9	110.4
Ssc.24179.1.A1_at, CK457041, ARF3	333.1	404.6	635.6	83.9	184.3	1129.6	394.7	199.4	1216.2	320.2
Ssc.27062.1.A1_at, CN166215, ZNF716	251.8	254.0	321.8	349.9	360.5	203.4	190.4	228.6	98.2	215.8
Ssc.23997.1.S1_at, CK452035, CNTN1	98.2	136.2	270.5	159.5	73.9	74.6	59.7	83.2	55.7	187.4
Ssc.5113.2.A1_at, BQ602388, C2orf67	228.3	159.0	132.6	529.1	147.5	68.2	84.6	99.1	30.4	73.5
Ssc.10086.1.S1_at, CF794789, SNX7	344.7	439.5	408.8	343.7	452.4	410.2	253.5	192.2	167.6	266.6

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
177.4	46.3	31.5	139.8	101.0	55.7	155.5	97.1	92.0	96.8	56.4	57.8	0.591166259	0.947352153
988.6	988.7	777.8	1667.9	1035.8	1346.0	1862.8	1198.7	1134.1	873.3	347.0	319.0	0.608845656	0.946104521
368.4	458.5	340.2	508.6	419.5	297.1	697.4	421.6	398.7	211.6	120.7	78.4	0.571685975	0.945632925
523.8	195.3	306.6	243.7	257.2	498.5	187.9	357.4	337.5	64.5	164.5	139.3	1.796639341	0.944261041
1853.6	2029.6	1766.8	1772.3	1518.7	1472.2	2926.8	1838.1	1735.5	255.5	444.8	209.3	0.592983871	0.9442099
773.1	1009.2	477.9	1222.6	1028.5	846.1	1451.2	950.0	892.9	462.6	326.3	256.7	0.615292383	0.939914525
472.2	376.0	367.1	199.2	241.9	453.3	230.8	374.3	351.6	89.1	140.3	110.4	1.523337088	0.939297608
311.5	273.4	222.0	376.1	207.0	318.4	463.5	303.4	284.7	163.6	109.2	63.7	0.614311399	0.938536928
21.3	15.9	23.0	20.0	9.8	53.8	38.6	25.6	24.0	16.9	8.5	15.4	0.621219976	0.937663015
62.8	45.9	47.5	35.4	48.6	42.2	78.2	50.3	47.1	23.9	8.8	9.1	0.60172164	0.9349755
175.9	183.4	210.2	191.3	192.6	224.7	328.9	211.0	196.4	126.0	90.2	18.0	0.596917371	0.930656934
213.3	288.0	213.9	241.2	163.7	147.7	416.4	228.3	211.3	114.1	98.0	51.2	0.507444765	0.925536575
2432.0	2385.1	1791.0	2261.3	843.5	1081.3	3055.8	1944.8	1799.0	1062.6	254.0	690.8	0.588723594	0.925057504
124.4	158.9	127.4	63.1	85.9	74.1	195.7	114.3	105.6	51.7	24.8	37.0	0.539661456	0.924499679
118.8	182.8	111.9	131.5	121.2	208.0	241.4	157.9	145.7	80.9	45.3	39.8	0.603562552	0.92296972
30.0	74.3	37.6	107.2	24.8	165.9	176.3	79.6	73.3	66.2	29.9	55.2	0.415815748	0.921317245
200.0	577.8	92.8	173.0	76.2	995.8	132.8	382.7	352.6	77.9	264.0	364.4	2.655120482	0.921252025
487.1	377.3	286.8	369.4	216.7	344.0	628.2	376.8	346.9	176.1	103.0	91.3	0.552221302	0.920505608
183.2	196.2	157.3	185.5	92.7	145.8	282.4	174.0	160.1	48.9	35.2	38.0	0.567065684	0.920422319
585.1	421.4	330.8	1117.0	164.3	290.7	976.5	527.4	484.9	391.7	136.7	340.0	0.496552313	0.919349538
438.9	384.5	267.4	446.8	395.7	182.3	918.8	383.6	352.6	327.7	115.3	105.3	0.383761428	0.919234579
48.2	83.4	67.1	84.1	72.9	30.8	118.5	70.2	64.4	35.7	21.3	21.1	0.543417131	0.918139491
562.6	407.5	359.2	237.9	298.8	472.2	279.0	424.5	389.7	32.2	129.7	117.7	1.396573968	0.917934706
310.7	212.4	76.6	288.8	135.4	54.0	500.8	196.0	179.7	330.8	74.7	108.2	0.358697388	0.916675171
424.4	503.2	298.1	341.8	229.0	269.7	653.0	375.9	344.4	72.2	89.8	102.6	0.527393204	0.916014967
267.8	266.7	176.4	274.2	222.6	148.8	388.8	247.2	226.1	88.6	17.7	53.2	0.581460144	0.914650592
296.1	306.3	248.8	264.4	659.8	186.8	539.4	357.7	327.0	81.9	119.5	168.4	0.606245983	0.914318199
25.5	31.3	21.6	28.5	22.2	7.3	39.2	24.9	22.7	17.1	6.3	8.4	0.579931973	0.913719185
1352.4	999.8	963.3	528.3	811.1	1573.1	625.3	1136.9	1038.0	107.8	452.4	375.1	1.660003198	0.913025121
692.6	470.9	506.7	264.7	758.0	347.4	332.9	555.2	506.7	152.5	85.6	191.3	1.522220219	0.91270699
1769.3	2434.6	1536.3	1960.6	1048.8	1190.8	2746.7	1816.4	1656.7	717.2	546.3	512.1	0.603181076	0.912117275
309.5	370.2	230.2	301.7	230.9	228.3	505.2	305.6	278.5	85.1	103.7	58.4	0.551157206	0.911093661
21.1	24.2	13.3	21.5	22.6	18.6	36.0	22.2	20.2	11.5	6.7	3.9	0.561886233	0.910660661
71.9	69.8	87.4	68.6	55.3	41.0	109.5	72.2	65.7	25.0	15.8	15.8	0.599586073	0.90976263
149.4	124.4	84.7	104.5	125.6	124.6	199.4	130.8	118.9	63.6	41.9	22.0	0.596181496	0.908905541
365.1	442.0	235.4	178.5	485.6	202.6	575.9	350.4	318.2	204.7	137.8	130.6	0.55256486	0.9082087
79.7	72.5	52.1	47.9	92.3	43.9	119.1	71.3	64.7	30.9	26.0	19.6	0.543703455	0.907900888
387.9	311.7	282.9	322.9	306.6	264.0	220.2	344.9	312.7	40.3	65.0	42.6	1.419921284	0.906595531
1061.7	801.7	785.6	672.8	466.4	680.2	1510.3	822.3	744.7	448.4	235.4	196.1	0.493115976	0.905715143
68.5	99.8	54.9	71.3	54.4	68.0	116.1	76.8	69.5	27.7	27.9	16.5	0.598581438	0.904966571
998.6	579.9	746.7	438.7	510.9	729.2	477.6	738.3	667.3	138.2	250.9	202.1	1.397264098	0.903927252
461.2	236.1	348.6	245.6	254.6	434.0	228.0	365.2	330.0	29.1	59.5	100.0	1.447187628	0.903561129
133.7	252.2	154.0	170.0	133.1	154.8	299.8	184.4	166.3	90.9	66.3	44.4	0.554703135	0.901843818
161.8	126.5	87.4	106.2	124.9	94.0	202.3	129.5	116.8	41.4	35.7	27.1	0.577360356	0.901791229
3241.5	2455.4	2031.6	2708.1	2373.0	2473.0	4242.5	2825.3	2547.1	706.9	555.5	404.5	0.600377136	0.901526199
218.9	239.9	234.4	232.3	105.3	278.8	425.0	242.1	218.3	98.5	73.4	58.9	0.513592797	0.9014069
434.9	244.7	376.3	145.3	191.5	304.7	177.1	314.1	282.9	58.8	56.8	110.5	1.597041888	0.900611231
27.4	33.5	33.1	30.2	36.8	9.2	52.2	31.5	28.4	43.6	9.0	9.9	0.543839468	0.899957699
203.8	58.5	108.7	92.2	106.5	163.3	79.2	135.8	122.2	42.2	40.9	52.4	1.542898038	0.899607266
1964.4	3201.9	2817.2	2789.4	5893.6	3531.2	2417.5	3756.1	3366.3	1162.1	2790.5	1344.7	1.392464667	0.896208164
462.3	456.8	393.4	386.5	356.2	309.6	717.3	440.5	394.1	168.9	130.0	58.7	0.549483233	0.89482208
243.6	286.5	199.7	284.9	196.5	190.1	403.6	261.6	233.6	69.3	48.2	44.6	0.578609652	0.89291176
225.0	221.4	143.6	179.7	81.5	133.6	284.6	183.9	164.1	141.1	54.7	55.5	0.576715859	0.892514047
590.0	380.3	370.5	489.5	381.3	444.1	986.2	496.3	442.6	464.1	133.9	85.8	0.44881935	0.891761024
1140.9	1370.6	872.6	1228.8	1448.8	468.9	2204.5	1221.5	1088.4	783.2	655.2	364.0	0.493732517	0.891092081
252.7	32.2	95.2	122.3	71.6	122.5	242.6	130.6	116.1	109.6	36.5	75.1	0.478457396	0.888982488
814.7	311.8	433.8	240.9	246.0	1429.7	328.3	652.0	579.5	212.6	481.6	468.4	1.765103056	0.888750856
255.3	128.8	153.7	101.2	75.3	280.3	307.6	187.3	165.8	51.9	51.8	83.7	0.538903338	0.885127438
62.6	66.3	36.4	113.2	178.2	31.7	147.7	92.1	81.4	76.2	54.4	55.6	0.551266423	0.883630048
85.4	93.0	37.0	71.2	65.1	25.1	239.3	71.2	62.8	166.1	25.7	26.8	0.262432094	0.882518269
249.5	258.0	176.2	243.8	185.8	252.5	397.8	258.0	227.6	51.4	94.6	36.5	0.572201833	0.882231352

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.12078.2.S1_at, CF794011, SRP72	145.2	292.9	172.1	30.9	162.0	291.3	367.7	71.0	297.2	266.8
Ssc.6550.1.A1_at, CK462428, TSPAN7	338.6	748.3	359.9	307.5	825.0	241.9	214.3	185.8	195.5	132.5
Ssc.6903.1.S1_at, BF702446	2333.2	2183.4	2648.8	1395.1	1905.3	3414.9	3259.9	2052.2	3786.1	3255.7
Ssc.21302.1.A1_at, CF795369, ENPP6	1856.2	1793.7	1182.4	1856.2	1992.7	72.8	661.0	1820.8	444.4	1262.7
Ssc.30706.1.A1_at, CO949613, RABEPK	127.7	157.3	193.7	130.7	150.1	297.4	170.3	292.0	287.5	215.1
Ssc.61.1.S1_at, NM_214009.1, C3	2464.9	3378.4	1572.2	3367.1	4996.6	1654.5	864.0	1656.8	1122.4	963.4
Ssc.24221.1.S1_at, CK451013, BIRC6	490.0	668.6	522.9	1024.0	759.0	472.3	365.7	377.2	107.2	392.1
Ssc.11668.1.A1_at, BI183460, KPNA2	1409.0	1280.1	1685.4	1479.5	1230.0	1670.2	3273.0	2119.7	3042.8	2193.4
Ssc.29063.1.A1_at, CN165554, EEA1	313.2	127.0	143.3	95.8	159.2	192.2	286.4	379.8	263.0	180.7
Ssc.8594.1.A1_at, CO941957, BLNK	200.0	174.5	107.4	357.8	367.4	45.3	33.7	78.0	19.8	64.9
Ssc.24158.1.S1_at, CN167043, ATG4C	157.0	286.1	163.0	338.0	390.8	177.3	205.4	156.1	90.1	195.7
Ssc.1171.1.S1_at, BQ604405, VAMP8	2942.4	2983.7	2962.2	2802.2	2804.3	2029.1	1823.0	1920.0	996.5	2499.7
Ssc.22988.1.S1_at, BX672811, PCTP	425.9	823.4	344.6	593.3	1872.6	123.6	230.0	399.6	86.4	543.9
Ssc.30838.1.A1_at, CF792234, PHIP	731.1	984.0	705.9	1270.1	1405.4	481.1	556.6	962.8	314.9	840.0
Ssc.27018.1.S1_at, CN165637, LARS	166.3	103.4	168.7	59.8	78.9	314.1	183.1	94.0	360.3	172.8
Ssc.30557.1.A1_at, CO994073, ST8SIA4	138.9	83.9	55.2	267.4	177.5	18.1	54.2	77.0	45.0	100.3
Ssc.24679.1.S1_at, CK462508, MIB1	253.4	592.0	313.6	143.5	459.7	795.9	749.8	298.0	601.0	339.1
Ssc.22345.2.A1_at, CF792177, SPIN1	412.3	357.4	210.3	464.6	377.0	202.6	234.6	173.4	298.1	231.2
Ssc.28706.1.S1_at, BF075590, CBX7	809.6	917.4	605.6	1435.9	1268.8	462.7	154.1	408.5	129.6	520.6
Ssc.1600.1.A1_a_at, CK457588	233.7	345.5	213.0	404.2	279.0	343.6	119.6	144.3	127.1	129.2
Ssc.3889.1.S1_at, CN158513, TOP3A	626.9	511.6	552.2	681.8	797.5	489.7	428.1	449.0	242.2	450.2
Ssc.4012.1.S1_at, CK466833, MFSD10	1842.4	1951.3	1473.5	2179.9	2109.3	1350.1	864.0	1361.4	661.6	1578.1
Ssc.6365.1.A1_at, BQ602340, C6orf98	435.4	467.1	237.6	589.1	633.3	251.2	251.0	413.2	143.0	306.5
Ssc.5509.1.S1_at, BF194181, ARL4A	1991.9	1590.6	1201.6	1774.9	1474.1	690.5	650.7	1247.5	619.8	926.2
Ssc.11005.1.A1_at, CK455895, GAB1	625.1	947.6	710.9	946.6	973.5	528.1	808.1	608.9	338.7	503.0
Ssc.14287.1.S1_at, CK457076, ABCC1	456.9	559.1	550.7	388.6	503.5	909.3	1030.9	607.5	848.2	823.5
Ssc.26200.1.S1_at, BX919092, THRB	253.3	195.0	161.5	336.0	252.4	83.7	132.3	122.9	133.1	163.0
Ssc.7688.1.A1_at, BI400970, ACAT1	880.5	869.5	711.2	1108.2	1247.8	653.8	579.3	710.0	371.9	788.9
Ssc.1119.1.S1_at, CN163605, MCCC1	353.1	514.9	315.8	443.5	642.7	271.0	239.2	206.3	175.1	288.4
Ssc.16338.1.S1_at, AF403246.1, ABCC1	194.2	178.5	168.2	54.3	154.5	301.1	342.2	142.2	178.0	240.5
Ssc.14361.1.A1_at, CF365719, OLFM1	485.5	319.9	442.7	357.8	403.1	266.3	245.5	275.2	206.4	247.5
Ssc.24549.1.S1_at, CK459975, LIG1	202.5	180.0	194.7	284.5	325.5	158.0	143.3	183.9	89.4	177.4
Ssc.8297.2.A1_at, BF712812, GPM6B	393.2	381.1	476.8	1272.4	791.2	580.5	339.5	451.1	223.0	251.6
Ssc.22154.1.A1_at, CF787551, DLG2	1233.2	1540.5	1673.8	1470.9	1439.3	741.9	759.2	767.1	845.5	888.1
Ssc.5077.1.S1_at, CF793055, NDRG3	418.4	367.7	314.3	458.0	483.3	225.9	212.3	314.2	184.3	319.0
Ssc.8830.1.A1_at, CN164417, DNAJC6	96.3	105.4	104.4	199.4	199.9	57.7	109.7	82.9	56.9	57.6
Ssc.19578.1.A1_at, CF368957, CTSO	175.9	249.6	112.0	431.2	564.4	128.2	61.0	163.1	88.5	207.7
Ssc.4443.1.S1_at, CN163832, ZNF598	1120.3	1054.9	1255.0	702.4	841.6	1610.4	1501.2	1202.3	2322.5	1208.0
Ssc.2114.1.S1_at, CF787850, TNRC6C	1833.7	1543.5	1365.1	2635.6	1811.7	1197.4	916.1	1567.8	751.0	1459.3
Ssc.29492.1.A1_at, CO956576, ANK3	635.2	902.9	727.4	1390.6	996.4	562.2	462.4	525.9	126.3	475.3
Ssc.19612.1.S1_at, CF175414, ABCC1	593.6	474.1	675.4	361.4	487.4	833.8	796.2	748.1	792.1	791.4
Ssc.494.1.S2_at, CK463653, KCNT2	59.6	15.6	64.0	26.8	36.0	118.0	38.2	52.3	36.0	60.4
Ssc.16088.1.S1_at, BP436947, HMGCR	115.8	138.6	198.4	34.0	114.2	196.7	231.6	57.6	262.9	166.7
Ssc.12764.1.A1_at, BI403538, C6orf1	176.6	178.1	165.8	355.6	232.7	125.3	153.6	190.9	114.3	147.5
Ssc.11004.1.S1_at, CN162228, C1QB	2741.8	2369.2	1583.9	5643.6	6063.8	1505.9	824.1	2805.1	1021.9	1304.0
Ssc.7021.1.A1_at, CB479037, EPB41L2	1477.9	1894.0	1667.1	2444.9	3046.3	1764.3	1342.0	1423.7	894.6	1423.3
Ssc.5274.1.S1_at, BI181700, RGS10	141.1	117.1	161.1	278.2	328.8	87.5	75.4	90.7	77.6	64.5
Ssc.21587.1.S1_s_at, BX667225, BRCC3	516.5	515.2	393.9	583.4	676.1	249.8	350.2	335.2	231.2	514.4
Ssc.2243.1.S1_at, BG608510, C20orf72	169.2	171.1	123.7	262.0	239.9	120.5	114.2	139.8	78.6	122.2
Ssc.11229.1.S1_at, CK464613, TMEM219	320.0	291.1	254.9	316.2	380.6	210.0	153.7	221.9	127.4	276.5
Ssc.27555.1.S1_at, CN153803, EXT1	552.3	467.4	562.2	329.0	349.1	528.0	711.9	625.3	1069.0	760.4
Ssc.2634.1.S1_at, CK457748, C14orf21	463.0	513.8	559.9	321.2	421.4	614.3	707.2	653.6	961.2	574.3
Ssc.9560.1.S1_at, BF702240, ABLIM1	2409.2	2233.7	1848.1	3210.4	3074.7	1027.1	1271.4	1905.1	1290.9	2294.0
Ssc.10300.1.S1_at, CK459802, KLHL13	935.4	992.4	468.1	1076.1	994.7	492.5	414.7	608.3	488.9	726.5
Ssc.27533.1.A1_at, CN164599, ZFP106	44.9	62.7	58.5	34.0	62.8	123.3	149.2	22.2	40.8	78.1
Ssc.21579.1.S1_at, CF789025, RGL1	440.6	603.6	354.3	372.1	931.3	146.1	277.9	205.0	128.1	233.2
Ssc.20419.1.S1_at, BX917576, SLC25A27	198.5	110.6	109.4	118.1	160.6	74.3	76.1	91.9	34.3	83.4
Ssc.20770.1.S1_at, BX676204, NSD1	212.7	247.0	219.9	389.0	250.0	223.3	169.9	193.0	96.1	129.8
Ssc.3649.1.A1_at, BQ602486, RCAN3	598.8	666.0	522.2	956.8	746.6	372.6	416.0	623.8	186.4	678.1
Ssc.4511.1.S1_at, BI401829, DHRS3	922.9	1262.4	376.4	1002.0	1489.4	224.2	248.8	618.7	230.6	624.4
Ssc.27799.1.S1_at, BG383975, EFNB2	2281.2	2235.6	2186.8	2415.2	2271.1	1522.2	921.1	1496.8	869.8	1691.0

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
286.1	157.0	179.9	236.0	177.3	330.7	160.6	258.8	227.8	93.1	111.5	69.2	1.418461794	0.880345183
288.3	131.6	120.8	238.8	75.2	169.5	515.9	194.0	170.7	249.4	40.5	79.5	0.330903734	0.879896907
3805.7	2230.7	3205.7	1916.3	2012.1	3472.9	2093.2	3153.8	2773.9	473.6	652.5	818.6	1.325221197	0.879553295
824.2	1154.7	740.7	665.8	283.7	828.3	1736.2	852.3	749.6	318.0	692.3	282.9	0.431718349	0.87942214
202.0	161.5	245.7	157.8	243.6	321.4	151.9	252.5	222.0	26.5	56.9	61.8	1.461487821	0.879347223
2105.4	400.4	541.5	2215.1	837.3	500.5	3155.8	1252.2	1100.0	1271.6	379.6	834.8	0.348570692	0.87846651
277.8	353.0	209.2	271.2	564.5	123.1	692.9	342.9	299.8	214.9	138.2	150.8	0.432674268	0.874307378
3194.2	2199.9	1941.9	1305.1	1990.0	2268.2	1416.8	2459.8	2149.9	180.1	672.9	614.7	1.51742189	0.874000266
257.8	268.1	247.2	199.1	193.6	199.4	167.7	260.4	227.5	84.7	80.5	33.8	1.356787915	0.873716816
87.6	5.5	19.5	90.5	28.0	21.9	241.4	48.3	42.2	115.7	23.4	37.1	0.174661033	0.872293477
172.6	165.2	111.8	152.9	111.1	145.5	267.0	164.9	143.2	104.5	45.9	26.3	0.536307339	0.868198723
2063.1	1518.5	1454.1	1854.5	1198.7	1550.9	2899.0	1853.7	1606.6	88.6	545.0	306.7	0.554210246	0.866735719
243.0	313.9	247.5	385.4	162.7	84.8	812.0	276.7	239.6	620.6	192.6	106.5	0.295026849	0.865739068
600.9	661.5	614.0	578.4	508.0	309.2	1019.3	631.1	545.3	314.0	265.4	126.1	0.535007685	0.864127105
249.4	182.5	224.2	144.7	117.3	246.5	115.4	224.9	194.1	50.0	109.4	55.1	1.681684283	0.863203771
72.0	67.1	45.7	44.6	35.2	40.5	144.6	58.9	50.9	83.5	31.3	15.0	0.351708397	0.863034623
562.5	424.4	459.6	546.4	300.2	589.4	352.4	556.8	480.4	176.0	229.5	108.6	1.363116181	0.862879278
138.9	399.2	163.4	188.4	196.3	93.5	364.3	228.0	196.6	95.2	46.4	106.0	0.539681233	0.862429453
320.4	434.7	217.1	389.0	190.6	177.7	1007.5	335.1	288.3	339.3	181.0	109.0	0.286115578	0.860190988
159.8	142.0	133.6	179.7	165.2	108.8	295.1	172.8	148.2	79.4	95.9	25.4	0.5021802	0.857740989
467.1	383.0	308.3	405.3	258.2	296.6	634.0	411.8	353.1	112.6	97.4	78.5	0.556913775	0.857331326
946.3	1249.9	887.6	1152.7	870.8	873.3	1911.3	1163.0	996.8	278.1	383.2	163.7	0.521517866	0.857035585
286.2	250.2	171.7	291.2	291.7	106.3	472.5	273.0	232.9	154.9	98.3	77.2	0.49287478	0.853115002
744.5	896.0	617.3	704.8	456.0	807.9	1606.6	826.9	704.4	299.4	264.2	153.8	0.438446345	0.85183528
533.1	442.3	360.7	536.7	583.6	389.9	840.7	557.4	474.4	160.9	171.1	89.8	0.564244991	0.851125544
917.8	728.8	774.8	384.7	600.1	902.3	491.8	843.9	718.1	70.7	154.6	201.1	1.460231278	0.850930622
124.2	100.1	98.5	135.4	87.0	102.6	239.6	127.0	108.0	66.6	28.5	18.1	0.450536916	0.850131234
410.6	775.0	418.8	648.6	457.3	453.7	963.4	620.8	527.3	212.8	158.9	149.5	0.547344239	0.849468948
177.3	224.8	145.0	228.4	143.6	283.6	454.0	236.0	200.5	131.1	46.3	55.0	0.441519824	0.849364407
292.3	179.5	250.9	153.0	159.7	190.0	149.9	240.8	204.2	55.4	83.0	55.4	1.362100396	0.848145072
267.7	239.7	205.7	182.7	98.9	265.6	401.8	248.2	210.1	65.8	26.5	63.9	0.522772524	0.846361512
160.1	177.8	118.2	156.4	55.3	91.9	237.4	150.4	126.6	63.9	37.7	46.9	0.533257525	0.841866135
330.5	300.3	268.4	182.1	556.7	224.7	662.9	369.1	310.5	379.1	147.9	131.7	0.468292757	0.841008831
874.1	630.5	636.2	534.4	668.1	684.5	1471.5	800.4	671.3	160.9	63.2	112.2	0.456188755	0.838747564
211.5	264.0	199.3	190.8	236.9	159.0	408.3	251.1	210.3	68.3	61.6	36.7	0.514889553	0.837182448
82.8	76.6	56.5	73.5	38.1	38.2	141.1	73.0	61.0	53.6	23.3	19.7	0.432024383	0.835389254
71.7	87.6	140.9	153.5	95.2	101.1	306.6	129.7	108.3	187.2	58.4	31.9	0.353314635	0.835260858
1625.6	1259.0	1341.3	1002.0	1025.4	1590.5	994.8	1568.9	1307.3	221.4	457.9	267.5	1.314080656	0.833269594
1089.6	1145.8	879.9	1035.9	1115.1	622.4	1837.9	1178.3	981.5	486.6	347.3	199.4	0.534000392	0.832923145
343.2	387.6	300.5	242.7	703.3	171.9	930.5	430.4	358.2	293.8	174.6	185.2	0.384954326	0.832210399
929.6	564.5	764.2	427.4	504.9	764.7	518.4	792.3	659.2	120.3	30.4	190.7	1.27168615	0.832008111
45.0	47.8	75.6	14.7	62.3	58.6	40.4	61.0	50.7	20.9	33.4	20.8	1.254125413	0.83087351
225.1	112.7	120.1	79.2	77.9	297.2	120.2	183.1	152.0	59.0	78.9	89.2	1.264836384	0.83032951
121.8	137.3	130.7	120.7	79.5	137.1	221.8	146.3	121.2	79.2	29.6	21.6	0.54646164	0.828207582
1663.4	220.5	592.5	3477.3	831.6	598.9	3680.5	1492.2	1230.7	2032.9	778.9	1201.7	0.334387549	0.824755395
1184.4	975.3	867.9	1135.5	1432.3	1181.2	2106.0	1369.6	1129.4	638.6	311.4	194.7	0.536282945	0.824656707
86.8	21.7	59.2	93.4	65.8	63.4	205.3	79.1	65.1	92.8	10.4	25.3	0.316915132	0.821961082
353.9	262.5	266.3	341.4	216.4	215.9	537.0	336.2	276.1	103.5	112.3	59.6	0.514071481	0.821235919
120.7	114.0	93.4	89.6	43.5	105.7	193.2	115.1	94.5	56.6	22.5	27.6	0.489094799	0.821165769
173.5	194.9	170.4	183.9	125.3	126.9	312.6	197.9	162.5	46.1	58.8	29.5	0.519846856	0.821037561
708.0	650.0	572.6	533.7	679.8	491.9	452.0	738.9	606.0	109.7	204.7	86.2	1.340707965	0.820115845
847.6	484.6	688.3	416.7	385.1	626.1	455.9	702.1	574.7	91.6	152.9	178.4	1.260767195	0.818568526
1719.7	1891.5	1056.6	1393.4	775.1	809.4	2555.2	1557.7	1274.3	575.3	523.8	470.4	0.49869809	0.818054396
601.1	963.3	390.0	345.2	83.8	293.5	893.3	546.2	446.2	242.9	122.3	303.1	0.499417915	0.816855249
81.0	61.4	55.8	56.8	40.8	109.2	52.6	82.7	67.5	12.7	53.6	24.2	1.283758083	0.816005803
227.6	147.2	158.7	235.1	96.7	104.4	540.4	198.1	161.6	239.6	61.7	59.1	0.29907966	0.815998519
62.6	90.6	40.5	76.4	51.0	30.6	139.4	72.0	58.6	39.1	22.2	22.5	0.420371964	0.81412037
152.6	103.7	132.8	113.3	131.7	157.0	263.7	162.4	131.9	71.9	50.4	21.0	0.499962081	0.811784263
378.0	396.3	347.4	510.4	307.1	277.0	698.1	455.4	369.4	166.7	199.2	82.0	0.529117962	0.811117455
301.3	363.2	198.7	707.2	196.7	127.7	1010.6	389.3	315.8	419.1	212.2	209.3	0.312481447	0.811116248
1308.2	1143.7	1061.5	1225.5	973.5	612.7	2278.0	1300.2	1054.2	85.1	377.4	246.3	0.46277111	0.810797992

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.29289.1.A1_at, CO953222	121.8	135.8	132.9	139.4	106.4	66.4	87.6	89.4	53.3	120.7
Ssc.5829.1.S1_at, CK451184, C8B	349.9	482.6	369.5	983.7	593.1	352.5	303.1	372.9	175.9	538.5
Ssc.27946.1.S1_at, AW416141, PRCP	2576.2	3280.0	2443.3	3377.7	4350.4	1364.7	1533.3	3154.1	1674.5	2548.1
Ssc.9666.1.S1_at, BQ600276, BTG3	981.8	1342.3	1504.5	1170.1	1279.9	2213.2	2308.1	1785.1	2988.3	2010.6
Ssc.14132.1.A1_at, CK464652, SYNJ2	265.5	296.7	215.3	289.8	369.1	630.8	358.7	356.4	608.2	298.5
Ssc.28058.1.A1_a_at, CN032188, GJC1	90.7	30.0	72.7	51.1	41.1	59.7	118.6	216.3	129.4	50.8
Ssc.9560.2.S1_a_at, BX674789, ABLIM1	1691.1	1666.9	1219.8	1212.4	2433.4	746.8	808.6	786.1	822.6	1484.1
Ssc.3835.1.S1_at, NM_001001637.1, PDLIM3	582.7	868.8	453.7	626.2	1223.8	534.4	349.6	487.2	186.5	708.3
Ssc.4532.1.A1_at, CF789780, RCOR1	635.5	730.7	491.3	1319.1	900.8	376.2	428.5	743.5	224.1	690.7
Ssc.3129.1.A1_at, CK464603, HMGN3	3677.1	4285.6	2780.2	9947.1	5834.6	2318.9	1793.7	5559.1	1726.6	4341.1
Ssc.12715.1.S1_at, CN164024, C1orf21	325.1	316.3	439.1	308.6	250.6	339.1	149.3	184.9	91.0	282.8
Ssc.3221.1.A1_at, BF710464, ERC1	2837.1	3040.4	2660.1	4067.4	2742.2	2477.2	1452.8	2857.4	1089.1	2176.0
Ssc.20989.1.A1_at, BI181437, SLC40A1	3660.6	4979.6	2219.8	6406.6	3131.8	1663.2	1186.5	1537.5	944.1	1568.2
Ssc.30916.1.A1_at, CO947301, AMIGO2	135.4	67.3	146.2	153.2	217.0	236.7	259.5	367.3	109.3	147.2
Ssc.5854.1.S1_at, BF443689, EGLN1	2085.7	1779.8	2083.9	1836.2	2061.8	904.0	910.0	1605.3	632.6	1593.0
Ssc.24502.1.A1_at, CK457935, C9orf95	65.1	57.3	53.6	94.4	133.6	53.1	43.0	36.0	37.5	54.5
Ssc.23465.1.S1_at, CN159832, TJP2	191.6	157.1	120.4	130.7	79.7	146.7	186.0	188.4	420.2	140.5
Ssc.14334.1.S1_at, BQ601883, GPM6B	670.2	769.4	763.3	1476.1	1219.3	1066.6	592.1	583.2	362.6	371.4
Ssc.30882.1.A1_at, CO950728, C1orf58	1494.8	1628.1	1331.8	2070.1	1763.5	1082.2	1118.1	1114.9	927.5	1092.5
Ssc.26386.2.S1_a_at, CK459456, NIP7	222.0	190.5	213.6	66.1	186.1	313.0	392.7	164.9	613.4	203.1
Ssc.9951.1.A1_at, CN166129, GNPNAT1	881.0	1344.6	982.8	943.3	843.6	2130.7	1697.8	1187.6	1696.0	1050.3
Ssc.3755.1.A1_at, BQ603873, NDUFB5	1004.2	1186.5	924.4	1168.9	1273.2	569.3	668.1	825.5	367.2	791.7
Ssc.8739.1.A1_at, CK456018, NCAPD3	449.1	354.7	414.3	718.7	526.5	295.5	287.2	350.4	209.9	311.2
Ssc.19823.1.A1_at, CO947469, ABLIM1	1732.1	1573.5	1140.2	1543.2	2156.0	667.2	852.2	902.3	686.2	1539.2
Ssc.9607.1.A1_at, BF711037, RCAN1	116.9	175.5	248.7	44.5	99.0	326.8	546.2	153.6	537.0	119.5
Ssc.877.1.S1_at, CN165098, FAM33A	299.5	298.8	248.7	359.6	304.0	290.4	206.4	204.5	109.9	195.2
Ssc.24837.1.S1_at, CN160525, BOC	309.6	346.6	330.4	276.7	396.2	160.5	237.6	411.7	133.9	161.7
Ssc.5993.1.A1_at, BQ599456, FGGY	224.4	355.6	122.3	466.9	321.0	68.2	65.0	156.5	160.6	221.7
Ssc.28568.1.A1_at, AJ656018, PDE12	324.4	379.7	362.1	284.6	233.9	418.6	654.0	380.5	719.0	388.5
Ssc.11962.1.A1_at, BI186430, AKAP9	73.1	60.7	44.0	81.4	93.4	61.6	43.1	31.9	42.9	53.8
Ssc.4190.1.S1_at, CA779719, BMP2	507.2	403.3	513.1	175.8	324.7	420.8	705.6	347.4	1137.8	356.3
Ssc.3541.1.A1_at, BF703522, NOSTRIN	468.3	641.2	435.5	486.5	594.4	273.1	274.2	408.6	226.2	326.1
Ssc.19389.1.A1_at, CF359935, C15orf48	100.4	138.7	99.0	205.7	107.9	83.1	241.0	198.8	373.6	292.2
Ssc.11977.1.S1_at, CF365948, NXT1	1376.0	1069.9	1515.2	985.6	940.6	1727.7	1779.8	1612.6	2661.5	1703.8
Ssc.5706.1.S1_at, BF199160, ZER1	624.8	573.0	500.9	794.0	710.0	392.1	323.2	558.7	289.8	525.5
Ssc.12946.1.A1_at, CA779821, PIP4K2C	759.3	841.8	750.7	1292.7	821.8	429.6	395.2	1041.7	328.4	716.8
Ssc.9734.2.A1_at, CF180439	480.1	413.3	537.3	540.4	355.2	555.4	731.9	717.2	1182.7	606.1
Ssc.1097.1.A1_at, CK462321, IRF2BP2	961.2	1093.5	856.8	1306.1	1267.6	416.0	606.3	727.9	427.3	815.5
Ssc.7756.1.A1_at, CK460011, MATN2	1624.9	1301.3	1794.5	1952.5	1545.8	232.0	675.3	816.2	333.6	315.5
Ssc.7559.1.A1_at, BQ599268, PIP5K3	258.7	269.8	118.1	100.5	357.0	114.8	214.6	134.3	87.3	120.4
Ssc.9402.1.A1_at, CK456696, ARHGEF10	880.5	1226.6	808.7	1131.8	1108.5	659.6	753.7	699.1	436.0	859.8
Ssc.8493.1.S1_at, CB287089, IRF2BP2	712.1	755.6	737.9	762.8	1095.9	447.8	500.7	516.7	466.8	640.5
Ssc.1585.1.A1_at, BI405224, GPRASP2	332.6	341.1	290.3	562.3	554.7	299.9	234.2	308.6	117.5	349.3
Ssc.9311.1.A1_at, CN162655, PHLDA1	185.2	235.9	249.1	160.3	173.9	586.7	244.7	160.0	403.4	238.4
Ssc.8436.1.S1_at, BF710666, MGLL	310.2	543.8	227.4	509.9	301.5	1539.1	649.8	929.6	451.2	358.9
Ssc.18661.1.A1_at, CF360512	98.3	108.2	106.6	122.2	121.9	41.7	64.5	84.8	92.8	82.7
Ssc.3796.1.S1_at, BF702868, C16orf45	1108.5	671.3	945.5	1783.6	1568.3	652.8	552.5	1043.3	392.7	804.8
Ssc.22262.1.A1_at, CN154831, CDC25C	102.0	106.5	76.0	89.5	120.6	31.3	68.5	67.0	33.1	64.2
Ssc.20531.1.S1_at, CK465633	3706.3	3561.8	3649.3	7138.6	4676.8	3394.1	2083.9	2983.8	880.7	2518.3
Ssc.4571.1.A1_at, CK467072, GNPTG	648.4	703.6	577.2	646.1	736.1	328.3	412.2	444.4	411.1	504.3
Ssc.16759.1.S1_at, BP442182, LMAN1	411.0	414.6	403.2	313.8	327.7	634.3	771.6	379.9	652.0	470.8
Ssc.8766.1.A1_at, BQ600288, CENPE	55.4	39.1	27.8	57.2	67.8	194.4	258.2	32.4	86.8	42.6
Ssc.242.1.S1_a_at, NM_214068.1, FUT1	268.8	312.4	249.3	427.0	448.5	198.1	154.1	238.0	160.6	222.5
Ssc.11101.1.S1_at, CF363568, STK24	116.5	126.1	164.6	123.8	100.5	171.6	231.9	139.0	269.8	158.6
Ssc.26328.1.S1_at, NM_001001618.1, CCR5	191.6	254.1	184.3	610.4	693.8	144.5	96.3	147.9	112.1	106.0
Ssc.9626.2.A1_at, CF359651, RASGEF1B	228.4	267.6	152.4	203.7	311.2	142.6	112.6	137.1	69.8	87.1
Ssc.10620.1.A1_at, BQ597414, KIAA1370	60.4	57.6	16.8	40.9	54.2	38.9	19.2	47.2	25.9	21.7
Ssc.14592.2.A1_at, AJ653382, CLIC4	1792.0	2796.6	2797.7	2006.1	2080.9	4631.4	1780.8	1475.0	4585.5	4752.8
Ssc.23179.1.A1_at, CN165371, INPP5A	899.1	710.7	1564.5	844.2	876.0	975.6	432.7	606.9	508.0	681.3
Ssc.9766.3.A1_a_at, CK467393, AK2	538.3	498.1	614.1	558.1	316.1	824.0	1187.4	882.9	1007.9	663.9
Ssc.6265.1.S1_at, BF713306, C14orf37	66.8	98.9	162.8	100.0	89.8	104.3	51.9	73.6	45.0	59.2

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
83.9	70.2	59.7	63.0	62.4	66.7	127.3	83.5	67.7	13.4	25.7	8.8	0.531588873	0.810373742
336.1	340.5	224.3	316.5	183.5	293.3	555.8	348.6	282.4	258.3	130.9	64.3	0.508073029	0.810048387
1996.9	1981.8	1854.7	1680.0	808.8	1656.4	3205.5	2054.9	1663.1	762.1	765.6	442.7	0.518823779	0.809318034
2171.3	1579.1	1640.2	1532.3	1375.1	2678.0	1255.7	2261.1	1829.3	195.2	453.5	496.0	1.456800348	0.809060057
393.1	246.6	457.0	345.7	374.1	369.6	287.3	450.5	364.4	55.8	156.3	68.9	1.268274854	0.808732132
86.9	96.4	118.6	48.5	143.5	62.8	57.1	115.0	92.8	24.5	66.4	35.1	1.624358077	0.807092322
945.0	1161.6	689.2	775.8	405.1	514.5	1644.7	929.6	748.5	498.0	311.3	277.9	0.455112927	0.805186237
399.0	479.3	262.3	390.3	346.8	309.0	751.0	453.2	364.5	304.0	196.7	76.0	0.485260439	0.804170344
398.9	441.4	326.8	550.3	432.6	224.6	815.5	492.6	395.8	318.4	219.1	110.8	0.485317441	0.803424009
2349.9	3328.5	2348.3	2752.0	1717.5	2651.6	5304.9	3147.9	2524.6	2823.7	1716.0	534.2	0.475904129	0.802010665
209.8	161.9	162.4	114.4	203.4	154.4	327.9	209.4	167.7	68.7	100.5	35.0	0.511424854	0.8008627
1471.2	1656.3	1602.7	1468.7	1730.0	1722.0	3069.4	2010.5	1608.5	575.6	728.4	116.9	0.524031528	0.800041449
1261.3	1342.4	645.0	1975.0	1165.5	228.4	4079.7	1379.9	1102.9	1639.9	303.3	603.5	0.270348001	0.799284972
130.5	114.8	145.2	120.8	398.7	163.5	143.8	224.0	178.9	53.3	101.3	109.1	1.244031892	0.798735119
960.1	959.0	1012.3	1009.1	804.0	658.9	1969.5	1129.0	900.6	149.1	443.6	140.7	0.457261138	0.797681683
26.8	51.7	28.5	32.2	26.9	48.2	80.8	44.8	35.7	33.6	8.6	11.3	0.442037954	0.796891269
151.6	157.4	206.9	116.5	165.6	232.8	135.9	216.4	171.8	41.8	116.0	41.6	1.264164827	0.794046959
436.5	451.8	377.3	330.7	750.3	485.2	979.7	595.2	472.0	350.2	285.7	147.1	0.481765783	0.792981395
921.1	1047.2	650.4	962.7	787.6	697.4	1657.7	1067.0	844.4	280.6	79.4	157.1	0.509392758	0.791348028
390.3	164.4	251.4	143.7	138.2	513.6	175.7	337.4	266.9	63.1	178.6	154.0	1.519602262	0.791101101
1316.1	939.5	1157.7	553.6	730.3	2671.1	999.1	1552.5	1228.1	200.5	436.3	759.1	1.229205453	0.791024683
575.5	587.3	435.2	590.2	500.9	368.8	1111.4	644.4	509.7	142.8	185.4	92.0	0.458549269	0.790939847
227.0	278.4	236.1	192.5	231.6	213.7	492.7	290.8	229.9	140.8	51.4	28.5	0.466616598	0.790411681
1011.8	1049.9	661.0	781.1	443.0	453.6	1629.0	929.4	733.4	366.6	355.8	263.7	0.450214856	0.789094274
312.2	123.4	241.9	42.1	187.8	685.1	136.9	336.6	265.4	78.0	203.0	225.8	1.938479891	0.78847563
181.2	190.5	150.2	115.0	115.3	198.7	302.1	201.3	158.5	39.3	64.0	37.4	0.524570811	0.787377451
182.3	244.2	171.7	147.7	165.9	131.6	331.9	221.1	173.9	44.4	113.4	38.9	0.523952998	0.786593088
84.1	131.2	75.4	232.6	63.7	46.1	298.0	134.4	105.5	131.0	67.1	68.5	0.354035253	0.785094246
484.4	420.6	444.3	300.5	317.0	443.7	316.9	512.1	401.8	59.1	161.5	75.1	1.26759008	0.784484105
34.3	40.9	41.0	36.8	23.1	43.1	70.5	46.7	36.5	19.0	11.4	7.3	0.518056343	0.782968996
598.3	253.6	513.3	209.8	226.9	975.0	384.8	593.6	462.8	140.6	337.4	298.9	1.202683506	0.779703943
239.1	363.6	230.3	275.7	146.3	155.1	525.2	301.6	235.0	88.1	69.5	80.6	0.447497366	0.779129647
83.6	25.4	52.4	58.7	34.4	856.5	130.3	237.7	185.2	45.1	108.2	329.5	1.420643445	0.778862062
2135.6	1328.2	1562.9	1144.8	1244.8	1442.0	1177.5	1897.1	1476.4	254.0	431.6	354.6	1.253871328	0.778239891
300.9	467.2	345.8	363.6	256.9	214.3	640.5	417.9	324.8	114.8	119.8	89.0	0.507046138	0.777253945
545.9	625.0	406.3	436.0	462.7	236.4	893.3	582.3	452.1	226.7	296.6	132.4	0.506067662	0.776264725
808.8	562.1	693.4	351.7	635.2	480.2	465.3	758.7	588.6	80.4	248.4	161.4	1.26502744	0.775797678
474.1	448.7	359.1	701.6	499.9	301.9	1097.0	598.6	464.2	193.0	177.8	138.1	0.42315382	0.775503954
635.9	712.4	137.7	408.4	173.6	136.3	1643.8	474.5	367.4	247.6	255.5	259.4	0.22349637	0.774220967
120.4	82.9	36.0	102.3	156.5	125.6	220.8	134.3	104.0	108.9	48.0	41.4	0.470745403	0.774128686
559.4	760.8	347.0	541.2	544.0	403.5	1031.2	681.6	526.0	177.8	156.6	144.1	0.510059283	0.771643878
392.0	417.9	381.9	450.1	395.4	343.0	812.9	514.5	396.7	159.4	75.5	35.9	0.488050423	0.771072238
193.5	219.7	184.7	173.8	154.2	284.1	416.2	261.9	201.7	131.3	90.7	45.8	0.484542688	0.770014
217.8	164.0	201.8	95.1	132.1	697.1	200.9	326.6	251.3	39.3	170.1	223.0	1.251078588	0.769399543
782.6	853.0	779.2	234.2	409.7	568.2	378.6	785.7	604.5	139.7	474.6	245.1	1.596796633	0.769336829
55.4	63.7	71.7	48.9	42.0	55.5	111.4	73.3	56.2	10.4	20.5	10.5	0.504307251	0.766712142
654.6	594.1	658.3	389.7	361.2	506.2	1215.4	689.2	527.4	454.9	248.3	130.2	0.433875798	0.765140304
40.3	35.4	18.3	66.2	50.9	31.1	98.9	52.8	40.4	17.0	18.9	16.6	0.408073864	0.764230721
1532.2	2040.5	1377.7	1864.7	2569.1	1491.3	4546.6	2372.2	1812.6	1517.9	967.9	446.8	0.398671376	0.764106693
371.8	509.3	248.7	290.5	284.3	216.9	662.3	420.1	320.3	60.9	63.7	106.2	0.483556804	0.762391087
518.9	442.7	425.9	234.7	299.4	739.2	374.1	581.7	443.5	49.1	155.6	177.6	1.185549555	0.762336978
139.7	108.8	12.0	118.0	164.8	18.0	49.5	122.9	93.6	15.9	99.2	63.9	1.891427416	0.761311849
127.3	226.4	171.9	94.8	76.0	192.3	341.2	194.7	148.1	91.4	37.0	58.5	0.434105119	0.760899346
196.1	158.7	166.2	89.1	111.6	164.6	126.3	194.2	147.7	23.6	54.7	39.6	1.169569807	0.760720294
154.6	42.2	58.2	192.1	70.4	36.4	386.8	121.4	92.3	245.4	23.4	65.0	0.238643022	0.760684465
94.4	80.5	88.6	112.3	77.2	48.1	232.7	109.8	83.5	60.6	31.4	21.3	0.35896444	0.760348386
21.9	35.1	15.7	16.3	38.3	12.2	46.0	30.6	23.3	17.9	12.0	10.9	0.505654632	0.76030085
2972.4	2045.5	1845.0	1639.0	3385.8	3798.4	2294.7	3445.1	2614.4	470.8	1663.5	893.5	1.139319115	0.75886041
442.8	543.7	488.2	366.7	704.5	367.1	978.9	640.9	485.5	335.4	209.7	127.5	0.495964859	0.757528476
926.2	462.2	619.5	343.6	460.1	1338.3	504.9	913.2	691.7	113.5	197.0	375.7	1.369766705	0.757375003
65.1	45.2	39.2	41.4	72.7	39.3	103.7	66.8	50.5	35.7	23.5	14.6	0.487008811	0.755738523

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.21555.2.A1_at, CN154463, BRF2	146.2	122.8	145.3	71.5	222.1	409.0	373.2	127.3	273.4	255.6
Ssc.235.2.S2_at, M20160.1, CAST	58.4	115.4	66.3	97.2	144.4	36.3	64.0	105.5	48.0	53.6
Ssc.19318.1.S1_at, BX670375, MTR	334.5	521.3	245.2	327.5	738.7	394.5	230.7	280.6	180.7	346.2
Ssc.1913.1.A1_at, CN163609, SLMO2	259.5	230.1	218.8	169.5	169.2	251.4	419.5	177.9	484.2	317.7
Ssc.6193.1.A1_at, CK451885	1957.8	1431.2	2255.2	1422.3	1815.9	1954.6	3258.2	2957.9	3607.9	2264.7
Ssc.1285.1.S1_at, BI399854, C3orf64	877.7	749.2	717.4	1209.5	1585.1	766.5	589.9	812.4	344.2	615.0
Ssc.9951.2.A1_at, BI399425, GNPNAT1	214.2	193.3	143.2	205.0	147.2	290.6	240.6	272.5	411.7	181.2
Ssc.27727.2.S1_a_at, BP173144, PGM5	649.7	858.8	446.1	445.6	951.5	258.2	338.0	243.5	221.3	416.9
Ssc.7256.1.A1_at, CK457247	1087.0	1693.0	615.1	1266.1	1939.5	578.8	375.5	976.9	594.6	1033.2
Ssc.30871.1.A1_at, BI118962, TP53INP1	110.4	91.9	149.8	249.9	440.0	126.5	81.2	98.0	79.1	73.8
Ssc.10905.1.A1_at, BF702853, PRR5	29.8	34.4	23.3	36.2	36.9	48.1	56.1	62.3	35.2	46.4
Ssc.1465.1.S1_at, BQ602989, DECR1	692.2	1063.1	537.3	1339.0	1057.7	638.4	524.4	605.9	399.6	695.8
Ssc.30548.1.A1_at, CO993702, ELMOD2	181.3	113.6	171.0	164.3	164.4	70.0	86.5	134.8	67.6	148.9
Ssc.20812.1.S1_at, CF359778, RFTN1	556.2	446.5	331.1	710.9	651.9	360.5	294.4	442.0	381.8	317.1
Ssc.17488.1.S1_at, CN164198	275.3	173.6	209.6	337.9	254.2	156.1	168.3	168.9	114.7	162.0
Ssc.21517.2.S1_at, BP437562, HNMT	199.7	317.1	284.0	77.9	368.8	351.6	572.5	216.6	409.3	328.3
Ssc.1206.1.A1_at, BM190132, ADAMTS19	860.8	1536.8	1334.5	1495.1	1593.2	559.4	669.6	1003.3	759.5	521.2
Ssc.8383.1.A1_at, CD572743, ANKRD12	324.1	387.2	287.0	482.5	334.3	183.2	178.3	219.6	163.3	338.0
Ssc.3452.1.A1_at, CF361112, DDX26B	320.9	375.9	212.0	442.8	434.7	166.5	233.0	230.2	120.2	230.5
Ssc.1560.3.S1_a_at, BI403714, RALA	2508.3	2519.4	2342.8	2040.2	1940.4	3376.0	4074.5	3173.1	4707.0	2430.6
Ssc.19836.1.S1_at, BF702104, SLC31A2	325.4	188.6	193.7	241.5	430.9	136.6	199.0	235.1	111.4	221.6
Ssc.1228.1.S1_at, CF175629, MARCKS	2638.7	2883.3	2913.8	3662.9	5594.3	2152.3	2101.1	2114.0	1268.3	1859.6
Ssc.25185.1.S1_at, CK465554, LIMCH1	834.2	446.2	788.2	326.0	586.8	436.2	151.9	234.2	175.0	356.5
Ssc.25174.1.A1_at, CF180708, CGNL1	942.0	768.7	520.1	336.1	1301.4	604.5	380.4	869.2	233.6	473.1
Ssc.29599.1.A1_at, CO941603, MCM8	55.1	58.3	28.4	78.0	32.5	29.5	25.2	30.2	26.4	36.8
Ssc.27746.1.S1_at, BE033068, SEMA4B	98.1	89.8	170.3	96.9	79.8	234.9	107.2	102.1	176.8	188.6
Ssc.7314.1.A1_at, NM_214321.1, PTGS2	847.8	917.0	1444.1	507.5	486.5	4801.7	1972.2	1350.0	4238.4	1039.3
Ssc.21267.1.S1_at, CN153804, NIPSNAP3B	852.7	755.4	693.4	1216.5	1191.0	695.5	472.5	410.5	230.0	623.2
Ssc.30689.1.A1_at, CO987866, CCDC82	551.1	646.9	466.3	1099.7	528.0	457.0	342.6	352.8	234.1	344.3
Ssc.29658.1.A1_at, CO942358, ICK	728.7	795.1	745.6	1065.6	955.6	496.8	500.6	467.9	530.1	649.6
Ssc.10536.1.S1_at, CF791997, LYAR	202.1	174.3	238.7	120.1	116.7	349.0	394.2	186.1	333.6	147.3
Ssc.2048.1.S1_at, BI186194, TIMM17A	1152.7	825.7	1245.4	554.8	844.6	1601.3	1393.7	1176.6	1956.3	1339.1
Ssc.29392.1.A1_at, CO954737, KLHL24	103.4	76.8	91.6	102.8	164.2	46.1	49.0	42.3	33.6	51.2
Ssc.18878.1.A1_at, CF365134, C5orf41	1088.8	989.8	434.7	531.9	739.6	236.4	535.2	605.2	349.3	528.8
Ssc.20196.1.A1_at, BX676761, COQ6	57.8	56.8	38.8	80.8	68.2	46.1	32.5	33.8	27.5	50.3
Ssc.11815.1.A1_s_at, BI184933, LAMA2	125.9	178.9	88.1	119.7	96.1	55.3	49.7	71.7	84.1	60.7
Ssc.25218.1.A1_at, CF178718, IVD	72.6	100.5	77.7	60.7	136.4	75.8	38.1	52.8	36.7	50.8
Ssc.2947.1.S1_at, CN162531, RPS6KA1	243.6	215.6	201.6	304.0	411.7	188.9	150.5	229.5	163.1	120.2
Ssc.1501.1.S1_at, CK457691, CRELD1	564.3	536.3	497.8	644.3	743.0	408.1	273.2	441.2	220.0	447.8
Ssc.9637.1.S1_at, NM_213909.1, GLUL	293.8	557.1	536.6	298.1	596.0	252.2	283.9	256.3	370.9	353.6
Ssc.30752.2.A1_at, BI119523, IFIT1	294.4	328.1	251.9	480.7	374.3	169.7	105.7	260.1	235.7	358.3
Ssc.3509.1.S1_at, BE235252, HK2	155.1	169.6	153.7	121.1	246.7	59.2	78.8	66.5	85.3	65.8
Ssc.29782.1.A1_at, CO947041, ERC2	40.2	47.5	26.4	45.4	63.8	29.6	38.3	27.2	24.7	21.6
Ssc.1019.1.S1_at, BF713103, TOX4	226.4	287.5	200.5	100.3	214.8	392.2	364.9	136.6	379.1	312.9
Ssc.5982.1.A1_at, BF712591, IRF8	232.0	249.9	126.3	506.8	687.0	177.6	79.7	130.7	126.9	136.9
Ssc.23808.2.S1_a_at, CN153513, CLIC4	189.5	206.2	247.4	162.2	177.5	751.7	379.0	191.5	657.2	253.0
Ssc.20618.2.S1_at, BX674463, EXOSC9	336.6	398.1	321.1	108.5	288.1	455.1	534.9	157.9	908.4	584.7
Ssc.18606.1.A1_at, CF368180, AP3B1	34.7	25.5	25.8	35.1	45.7	50.5	45.7	49.4	56.4	70.5
Ssc.16894.1.S1_at, BQ598284	5701.7	6408.3	8579.8	2094.8	3575.2	13894.0	7248.8	6529.4	12938.1	5296.7
Ssc.10047.2.A1_at, BI400278, BRI3P1	106.6	123.4	94.0	138.1	145.2	92.4	83.5	91.6	53.6	79.7
Ssc.9986.1.A1_at, CN157453, NFIA	5732.9	6061.0	4919.5	8763.3	6714.8	4051.3	2968.8	6883.8	2357.6	5096.0
Ssc.24966.1.S1_at, CK461742, NP	2973.6	1557.7	3308.1	878.4	1343.8	2951.2	3882.8	2473.6	4710.4	2431.2
Ssc.4373.2.A1_at, BI400843, DOPEY1	325.2	392.0	421.3	670.8	361.1	178.3	278.7	317.5	284.6	309.6
Ssc.1248.1.S1_at, BG383179, SPINT1	959.0	1045.2	1010.4	1369.1	796.0	907.4	373.9	918.9	418.7	809.0
Ssc.29991.1.A1_at, CO939836, PPP2R5C	66.1	54.9	25.0	71.1	33.9	22.9	24.9	56.1	17.1	40.4
Ssc.24984.1.S1_at, BX919125, NAAA	171.5	185.1	316.7	317.5	356.0	243.3	105.8	170.2	85.0	131.2
Ssc.6694.1.S1_at, BQ602470, CYCS	1257.9	1014.3	1303.7	737.9	717.8	2403.2	2081.5	1383.5	1747.1	1882.3
Ssc.14232.2.S1_at, BX674666, SYNCRIP	1590.7	1364.6	1148.4	561.9	927.1	1876.1	1772.5	2649.5	2346.2	855.7
Ssc.28609.1.S1_at, AJ659067, CABLES2	382.8	358.2	372.3	268.2	352.8	582.8	639.3	494.1	1069.6	651.2
Ssc.1339.1.A1_at, CF175557, SMARCA2	2184.5	2402.2	2033.7	5025.5	3171.8	1779.2	1100.3	2103.3	625.1	1981.7
Ssc.25067.1.S1_at, CO987060, PDGFC	1344.0	2148.0	1209.2	2451.1	2845.2	871.3	932.8	1510.4	806.0	1179.7

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
242.5	245.2	222.8	197.5	199.4	194.0	141.6	287.7	216.9	54.3	110.7	23.2	1.531996045	0.753910323
35.1	60.3	48.4	48.6	25.6	60.0	96.3	61.5	46.3	35.4	26.6	13.8	0.480935575	0.753632618
219.5	289.2	207.7	282.5	115.3	179.1	433.4	286.5	215.6	198.3	86.0	65.4	0.497300664	0.752250995
422.7	236.8	319.9	101.7	165.0	242.9	209.4	330.1	248.2	39.5	123.7	113.3	1.185018941	0.751701298
2737.4	1972.5	2318.4	1594.3	1450.5	2593.9	1776.5	2808.7	2111.2	356.5	687.1	527.4	1.188398781	0.751663308
398.2	579.2	411.6	658.8	308.6	463.2	1027.8	625.6	469.9	367.5	183.9	128.2	0.457231444	0.751172208
222.8	203.6	224.5	76.0	128.0	403.8	180.6	279.3	209.8	33.2	84.9	111.9	1.161719644	0.751050169
256.7	294.9	193.5	349.3	103.9	132.6	670.3	295.6	221.8	232.3	80.8	95.4	0.330901731	0.750445452
529.1	820.8	483.8	818.9	245.4	305.2	1320.1	711.8	533.9	518.9	282.0	245.6	0.404401553	0.750023415
89.4	74.5	57.1	66.2	84.5	41.0	208.4	91.7	68.8	143.2	21.4	18.0	0.330054383	0.749927315
18.2	39.4	22.6	47.8	71.5	23.3	32.1	49.6	37.1	5.7	10.3	20.3	1.156081362	0.748354158
335.7	773.0	313.5	470.2	312.8	366.6	937.9	572.8	428.6	320.8	115.0	178.6	0.457033388	0.748286256
76.3	85.9	68.7	69.6	59.3	95.3	158.9	101.6	75.9	26.3	37.8	13.0	0.477284168	0.746849153
313.5	258.5	242.4	339.1	184.2	271.1	539.3	359.2	268.1	153.6	57.7	54.6	0.497169275	0.746556781
137.0	128.2	117.6	83.8	87.5	135.0	250.1	154.0	114.9	63.0	22.6	23.6	0.459179594	0.745779221
354.8	280.2	245.9	221.1	195.6	382.7	249.5	375.7	280.1	113.9	130.4	74.7	1.12244489	0.745487941
478.5	320.6	399.9	411.6	548.4	972.8	1364.1	702.6	522.0	297.3	192.5	233.9	0.382651066	0.742907297
183.3	123.5	160.5	130.4	230.4	134.2	363.0	216.5	160.4	75.8	71.0	40.9	0.441803023	0.740869056
170.0	212.6	124.8	152.4	120.1	90.7	357.3	196.1	145.1	95.0	50.9	43.0	0.406146784	0.74000408
3324.3	2926.2	2742.5	1852.8	1795.9	3103.4	2270.2	3552.2	2624.2	267.3	871.7	649.0	1.155915873	0.738740438
164.1	151.3	111.2	169.3	64.4	140.4	276.0	180.7	133.5	102.5	54.1	39.6	0.483479458	0.738353436
1584.3	1171.1	1148.2	1585.3	1362.8	1546.3	3538.6	1899.1	1399.7	1211.5	371.0	203.4	0.395542493	0.737031303
194.7	245.5	195.0	171.6	248.9	140.5	596.3	270.8	199.4	217.4	121.8	42.1	0.334350752	0.73632245
537.5	483.9	316.2	427.2	208.4	283.9	773.7	512.2	376.2	375.0	241.1	126.9	0.486238572	0.734503541
11.3	28.9	22.1	29.0	12.0	27.1	50.5	29.6	21.7	20.3	4.5	8.2	0.430704188	0.733738465
132.4	141.4	123.2	63.5	114.0	137.6	107.0	161.9	118.7	36.1	56.6	28.8	1.109397395	0.732975132
2410.0	1158.5	1947.1	360.6	1372.3	4485.4	840.6	2680.3	1955.7	389.4	1724.2	1423.1	2.326548336	0.729633029
373.0	366.9	322.8	321.5	329.7	413.4	941.8	486.3	354.6	245.9	183.1	36.5	0.37645997	0.729016737
245.7	382.0	211.1	269.6	217.3	188.0	658.4	346.2	252.3	255.1	78.9	69.6	0.383176387	0.728805562
370.6	464.2	321.1	364.7	540.0	251.6	858.1	529.0	385.4	146.6	70.9	102.8	0.44908249	0.728481411
340.7	160.5	198.4	77.5	125.9	328.8	170.4	282.0	205.3	52.7	108.5	108.0	1.204953633	0.727910935
1334.6	874.5	1127.7	716.9	779.5	1686.4	924.6	1493.4	1086.6	277.4	300.0	373.9	1.175160062	0.727601446
43.2	47.4	22.7	32.7	33.3	14.3	107.8	44.4	32.3	33.3	6.9	12.4	0.299430834	0.726072607
382.0	659.1	223.5	251.8	303.8	142.7	757.0	451.0	327.2	282.5	152.7	181.2	0.432189283	0.725420196
18.9	24.0	29.9	36.2	30.4	26.0	60.5	38.0	27.6	15.5	9.7	6.0	0.45579806	0.72467578
52.5	63.5	28.2	76.0	26.4	32.8	121.7	64.3	46.6	35.6	13.7	20.6	0.382509173	0.724209435
33.3	40.8	39.4	45.6	37.0	24.8	89.6	50.8	36.8	29.9	15.7	7.2	0.410992037	0.724167322
199.2	75.6	129.0	148.3	93.0	95.2	275.3	170.4	123.4	85.8	41.2	45.6	0.448177745	0.723910663
289.0	294.4	269.5	208.0	152.0	340.0	597.1	358.1	258.8	97.7	104.6	67.6	0.433427114	0.722830438
237.5	226.7	234.0	242.1	150.4	224.9	456.3	303.4	219.3	148.0	55.4	34.4	0.480510753	0.722745951
144.1	293.4	166.8	115.2	63.9	195.5	345.9	225.9	163.2	87.7	95.4	78.2	0.471695386	0.722222222
79.8	31.5	55.0	30.4	47.0	64.4	169.2	71.1	51.4	46.8	10.6	19.2	0.303415268	0.722019123
17.0	25.2	17.1	26.5	20.2	16.2	44.7	28.3	20.4	13.5	6.3	4.5	0.456038215	0.720179161
333.9	200.5	213.1	119.7	177.4	324.1	205.9	317.1	228.1	67.7	105.3	84.5	1.107900275	0.719293267
135.1	31.9	49.9	185.7	73.3	86.5	360.4	130.4	93.7	230.0	34.8	57.2	0.260081391	0.719034469
390.9	226.2	316.6	150.5	247.1	589.0	196.6	446.5	320.1	32.7	247.3	155.1	1.628256003	0.716829421
538.5	280.0	368.5	323.7	226.8	533.7	290.5	528.2	378.5	109.3	269.4	130.8	1.303130451	0.716647734
27.3	49.7	50.2	21.4	41.9	43.4	33.4	54.5	39.0	8.3	9.7	12.0	1.168565148	0.71529052
10179.1	5087.9	7571.6	3909.4	3529.3	8861.5	5272.0	9181.4	6523.1	2519.5	3942.7	2749.1	1.237326029	0.710472622
49.3	99.0	40.8	48.0	55.1	49.0	121.5	80.2	56.9	21.3	15.8	21.1	0.468192546	0.709414504
2995.1	4492.1	2748.6	3206.8	3032.7	1679.3	6438.3	4271.5	3025.8	1451.6	1796.7	902.6	0.469963603	0.708361622
3474.4	1281.6	3199.8	643.4	1625.9	3752.2	2012.3	3289.8	2329.6	1065.7	985.9	1306.0	1.157643913	0.708104346
212.1	145.4	195.2	198.4	196.7	215.1	434.1	273.7	193.8	137.1	55.8	25.2	0.446499877	0.708031952
570.6	522.6	456.8	464.4	621.1	274.6	1035.9	685.6	485.0	209.3	268.0	120.6	0.468189921	0.707454515
30.8	31.3	17.9	20.9	17.3	18.6	50.2	32.3	22.8	20.1	15.9	6.5	0.454183267	0.706319703
105.4	82.4	136.4	152.1	85.1	61.0	269.4	147.1	103.7	84.8	62.5	34.7	0.385110385	0.705189214
2249.1	609.2	1560.2	650.9	957.3	2006.5	1006.3	1899.5	1338.9	277.1	379.7	703.5	1.330458171	0.704844733
1673.2	1215.1	1594.1	960.1	965.1	1623.0	1118.5	1900.0	1338.4	397.1	683.4	333.5	1.196589602	0.704438596
643.3	402.2	549.8	386.3	417.1	506.3	346.9	687.4	484.2	45.5	222.5	100.9	1.395856157	0.704344874
1019.1	1422.1	750.0	1337.8	1171.3	709.9	2963.5	1517.9	1068.4	1233.1	632.0	296.9	0.360503542	0.703835951
897.9	818.4	678.6	1026.8	323.8	727.3	1999.5	1060.0	745.5	706.3	288.7	241.0	0.37282654	0.703243903

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.17287.1.A1_at, BQ598577, C5orf13	1178.8	1950.0	651.8	2125.9	2547.5	628.1	445.4	586.3	323.7	919.2
Ssc.4215.1.S1_at, BQ604532, TOR1B	318.7	293.5	327.6	388.7	315.7	382.2	612.7	466.8	686.2	552.8
Ssc.26621.1.S1_at, AJ659723, SYCP3	114.0	66.2	74.7	167.0	200.3	51.5	55.6	102.0	87.8	61.9
Ssc.24767.1.A1_at, CK464751, ACSS3	113.2	99.8	48.4	60.6	136.8	27.9	61.0	81.2	19.8	28.4
Ssc.9950.1.A1_at, CF792729, APP	1382.4	1505.5	1452.8	1528.1	1775.2	578.5	700.0	1355.5	742.9	1219.8
Ssc.5332.1.S1_at, BX673531, APOBEC3H	382.8	402.8	263.8	316.0	352.2	280.2	210.6	202.4	174.3	263.8
Ssc.30671.1.A1_at, CO947670, MPZL1	927.0	1023.0	1285.6	1068.9	1597.1	669.4	991.7	673.7	743.1	680.3
Ssc.5284.1.S1_at, CK464615, SLC25A4	735.5	874.6	721.8	957.9	1076.9	513.8	504.7	530.3	459.6	691.4
Ssc.17843.1.A1_at, CN161002, ANKRD32	318.0	399.8	259.5	576.1	529.0	184.6	164.3	200.0	93.8	244.2
Ssc.12421.1.A1_at, BI402162, NARG1	611.4	410.8	270.9	169.0	191.7	509.9	550.5	412.3	725.9	449.6
Ssc.2695.2.S1_a_at, BP157354, NCL	668.0	669.9	507.0	28.8	355.0	1054.4	870.8	254.8	1414.6	563.0
Ssc.15332.1.S1_at, BX914324, FAM46A	2251.3	1752.8	1949.2	1987.6	2141.1	1165.1	1004.2	1434.0	1366.2	1101.0
Ssc.27087.1.S1_at, CN166524, GOLT1B	246.9	267.8	228.5	147.4	175.3	381.1	531.2	189.0	653.3	280.8
Ssc.10946.1.S1_at, CK456879, NAT13	98.9	93.8	122.6	73.7	99.4	181.2	183.0	142.3	153.0	162.6
Ssc.17286.1.A1_at, CK460825, BTG2	2231.6	5631.5	3397.9	4569.4	4921.3	2762.5	1901.6	4284.4	1640.9	2983.5
Ssc.927.1.S1_at, BX927055, EYA3	39.0	29.8	72.8	81.7	74.6	60.8	148.1	120.4	56.3	93.2
Ssc.29702.1.A1_at, CO945041, PLEKHA3	638.2	531.6	566.2	531.4	426.7	638.8	1034.0	782.6	1165.3	669.7
Ssc.26819.1.A1_at, CN160586, FGD4	247.1	216.1	157.2	321.2	409.8	114.4	71.8	255.6	53.2	73.9
Ssc.13777.1.S1_at, AB032169.1	1876.4	2442.2	1250.6	3671.7	2727.8	1089.3	532.4	1791.4	1025.9	2327.8
Ssc.14444.3.A1_a_at, CN070640, ARG2	146.4	55.1	117.1	62.1	72.7	82.9	243.0	159.2	227.7	77.0
Ssc.29410.1.A1_at, CO955026, PLCB4	315.2	253.3	139.3	293.0	269.1	100.9	101.7	142.5	76.0	157.0
Ssc.15634.1.S1_at, BG384834, CSNK2A1	507.6	484.0	563.2	301.2	384.2	707.3	837.2	483.3	984.0	569.2
Ssc.8658.1.A1_at, BQ603433, PRKACB	1683.8	1523.0	1251.2	1857.9	1367.7	955.5	953.1	1139.8	626.3	1064.0
Ssc.6367.1.A1_at, BQ598231, C19orf15	171.7	187.7	171.6	307.3	283.0	179.0	112.5	207.1	86.0	117.4
Ssc.4792.1.A1_at, BF703643	135.3	131.6	135.4	210.5	242.1	67.7	77.0	137.1	74.1	96.6
Ssc.29774.1.A1_at, CO946659, PRKD3	165.8	117.4	52.0	46.3	134.7	132.4	156.5	233.4	275.4	95.4
Ssc.5182.1.A1_at, BF710924, IER3	538.2	990.4	754.4	1021.1	472.8	989.3	954.7	1948.4	1868.8	1049.9
Ssc.10801.1.A1_at, CF795118, C3orf58	1003.1	922.7	779.1	1233.7	1155.3	721.8	474.6	782.5	373.5	627.4
Ssc.8432.1.A1_at, CN163517, EXOSC4	741.6	447.6	684.4	371.5	346.7	685.9	874.1	957.6	1109.1	778.7
Ssc.19607.2.A1_at, CF368807, C1orf173	1391.1	1157.6	988.2	1553.4	1610.1	668.2	626.4	966.0	611.6	1223.8
Ssc.7460.1.A1_at, CO938496, IVNS1ABP	1668.2	2371.5	856.6	1847.3	2779.8	875.9	903.0	1096.3	1025.3	1492.7
Ssc.3189.1.A1_at, BQ600803, RCAN1	2343.3	3018.5	3743.1	2259.7	1812.9	3460.3	4724.0	5167.8	6271.0	3063.8
Ssc.29469.1.A1_at, CO956923, ATP2B4	412.5	289.4	364.4	194.7	168.0	646.6	263.6	223.9	668.4	404.2
Ssc.12162.1.A1_at, BQ603706, CHD6	258.1	255.0	239.1	499.4	320.2	172.3	161.4	275.7	138.0	270.8
Ssc.20974.1.A2_at, CB475108, GNS	1387.7	1778.2	1513.3	2614.0	2523.3	1272.4	1007.8	1592.6	854.0	1455.6
Ssc.8449.1.A1_at, BQ601482, P2RY12	226.7	147.7	87.2	397.5	213.5	49.0	48.1	57.9	28.5	27.8
Ssc.7580.1.A1_at, BQ599336, PLSCR3	631.2	536.7	501.6	738.1	738.6	359.8	318.1	557.0	312.9	403.9
Ssc.6441.1.A1_at, CO948967, DHRS7	503.4	479.0	353.3	517.7	386.1	251.4	238.4	241.7	235.1	488.1
Ssc.24468.1.A1_at, CK457493, NME7	133.6	88.8	78.3	136.2	167.1	48.0	55.2	85.3	52.4	106.6
Ssc.10437.1.A1_at, CO947417, SLC40A1	590.0	1253.5	491.9	1000.1	695.9	342.2	262.1	233.9	169.7	290.0
Ssc.21607.1.A1_at, CB472778, PPP2R2B	694.5	863.7	526.0	985.9	1909.9	620.7	196.4	304.5	303.0	106.2
Ssc.3080.1.A1_at, CN164821, ZNF251	248.5	259.9	364.6	483.8	511.0	294.4	246.1	250.6	116.0	292.9
Ssc.11669.1.S1_at, CN163190, EIF5A	2691.2	2241.8	2678.2	557.5	1743.3	3498.4	3568.5	2361.5	4580.9	2395.9
Ssc.2143.1.S1_at, BF441460	450.3	604.7	484.5	722.6	390.2	245.0	181.5	303.7	145.5	253.8
Ssc.13262.1.S1_at, BX924410, EIF4EBP1	897.8	573.8	997.0	475.1	544.9	994.6	1505.1	1210.8	2145.2	996.5
Ssc.13841.2.S1_at, BX926808, BZW1	1541.8	1879.0	1720.6	442.4	1349.3	2416.0	2764.5	1020.8	3167.5	1466.7
Ssc.5821.1.S1_at, CK462319, STIL	71.8	73.2	44.3	81.8	44.5	81.5	146.5	102.8	120.8	79.4
Ssc.829.1.A1_at, CK461725, LPIN2	746.8	768.3	681.9	706.6	561.9	1133.9	993.5	606.7	1666.0	930.2
Ssc.29071.1.A1_at, CO939249, CHD8	263.3	251.1	263.4	432.3	365.8	171.6	121.7	168.6	111.9	118.0
Ssc.9330.1.A1_at, BF710261, LCP1	351.6	334.2	441.8	1035.5	1031.8	173.5	135.7	412.2	282.4	142.5
Ssc.17585.1.S1_at, CD572095, LRRC45	641.3	508.6	454.3	476.5	666.4	345.3	302.8	335.4	339.1	431.9
Ssc.30461.1.A1_at, CO992095, DDX19A	228.1	210.1	176.0	233.0	198.1	127.3	45.4	212.9	114.7	137.5
Ssc.21696.1.S1_at, BF189187	641.7	505.0	622.2	427.7	392.8	760.3	794.0	923.9	949.9	642.8
Ssc.9108.2.S1_at, CF361753, WFDC1	2830.1	2654.8	3630.8	915.0	1859.9	5395.3	4305.8	2296.6	4854.2	3317.9
Ssc.27568.1.S1_at, CN163314, CEP250	108.9	112.3	95.0	134.3	210.1	84.6	92.1	103.1	49.5	93.4
Ssc.25680.1.S1_at, BX920706, MSH3	52.2	52.6	56.7	86.2	76.5	37.9	33.2	57.9	15.6	44.0
Ssc.8003.1.S1_at, BX666112, MTMR4	674.7	807.5	789.5	1415.8	878.7	743.0	605.2	604.1	328.8	675.5
Ssc.18132.1.A1_at, CN166082, HINT3	59.7	70.5	84.0	50.2	62.7	145.5	106.0	80.4	62.5	119.7
Ssc.18476.2.S1_a_at, CK450529, SSH2	635.3	846.0	517.0	1363.6	1707.4	508.8	581.6	739.6	549.2	469.6
Ssc.8582.1.S1_at, BF712824, PUS3	569.3	743.4	780.7	348.1	628.0	863.9	1203.5	546.1	1442.8	785.0
Ssc.20896.1.S1_at, AJ657042, PSMD7	2288.0	1795.5	2191.0	943.6	1228.4	2499.1	2942.2	2039.1	3991.1	1850.0

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
319.1	833.4	187.6	487.0	518.2	103.6	1690.8	580.5	408.2	763.6	224.3	264.0	0.241394606	0.703052331
422.0	448.0	349.1	280.7	342.5	430.6	328.8	540.1	378.8	35.7	119.5	65.1	1.151978673	0.701330519
40.8	35.3	27.3	85.4	58.2	54.8	124.4	71.8	50.3	58.2	22.0	20.8	0.404210865	0.700947603
16.6	43.2	27.3	33.3	30.5	32.4	91.8	43.7	30.6	36.8	26.3	8.7	0.33293374	0.699725149
818.2	644.2	566.8	602.7	601.0	626.1	1528.8	919.3	643.2	148.7	344.9	89.6	0.420700331	0.699596087
168.3	233.8	126.0	207.7	57.6	154.8	343.5	226.3	158.0	55.3	44.3	62.3	0.460041143	0.698459
659.2	614.8	473.7	529.8	364.6	498.1	1180.3	751.6	523.4	267.5	137.5	105.0	0.443410826	0.696299647
390.1	385.9	332.7	431.6	380.1	335.1	873.3	540.0	375.9	150.5	88.6	37.3	0.430435646	0.696193545
111.1	167.9	111.5	166.4	84.8	97.9	416.5	177.4	123.3	134.9	55.2	35.4	0.295972596	0.694929906
568.8	335.6	373.6	222.9	342.9	364.1	330.8	529.6	368.0	183.2	122.0	112.3	1.1125388	0.694780102
920.4	563.5	618.6	293.4	390.8	673.2	445.7	831.5	576.7	267.1	446.1	221.0	1.29369139	0.693489032
771.5	991.9	780.1	879.3	962.2	662.8	2016.4	1214.1	841.3	190.8	180.8	125.9	0.417228724	0.692941273
345.9	262.5	264.4	151.5	273.1	392.7	213.2	407.1	281.7	50.3	187.2	82.6	1.321340338	0.69196063
153.5	95.2	117.2	73.3	84.8	158.0	97.7	164.4	113.7	17.4	17.7	35.7	1.163663664	0.69131898
1536.8	1688.8	1883.0	1428.8	1221.5	3497.0	4150.3	2714.6	1876.0	1342.7	1043.2	825.4	0.452007145	0.691076827
74.0	20.6	49.3	52.2	171.7	29.1	59.6	95.8	66.2	23.5	39.2	55.0	1.110271903	0.690789474
922.8	690.0	616.3	368.4	473.3	482.8	538.8	858.1	592.3	76.3	231.6	197.8	1.099192062	0.690223134
105.6	75.6	48.7	113.9	94.8	32.4	270.3	113.8	78.5	97.9	82.4	32.5	0.290439544	0.689927931
1079.6	877.0	626.6	1406.6	392.5	1220.0	2393.7	1353.4	933.7	911.3	705.8	378.8	0.390066033	0.689924829
108.1	79.9	101.6	49.0	74.3	239.6	90.7	158.0	108.8	39.4	77.9	67.5	1.199272166	0.688465434
103.2	109.9	49.8	73.7	100.5	40.1	254.0	115.6	79.5	68.3	33.2	29.6	0.313148017	0.687885602
677.1	350.5	530.1	307.8	317.8	770.3	448.0	716.2	492.3	104.6	201.4	198.7	1.098711425	0.687331285
707.6	878.4	529.4	658.9	495.1	635.5	1536.7	947.7	650.8	242.4	196.1	137.3	0.423510247	0.686703808
95.9	125.5	85.5	97.3	103.5	70.3	224.3	140.4	96.3	65.6	50.5	18.4	0.429560926	0.686134853
62.4	68.9	41.8	78.3	59.2	61.7	171.0	90.5	62.1	51.7	28.2	12.1	0.362907942	0.685635359
131.5	176.3	125.8	97.5	136.1	65.5	103.2	178.6	122.1	52.4	74.0	37.5	1.182842567	0.683667376
595.5	866.2	794.9	404.0	661.3	2263.0	755.4	1362.2	930.8	251.4	500.7	672.3	1.232249552	0.683308619
479.4	489.1	333.8	446.0	418.5	276.5	1018.8	596.0	407.2	181.5	170.2	84.9	0.399710111	0.683295299
814.5	615.3	656.9	510.8	404.8	608.4	518.4	881.1	601.8	182.7	163.2	138.3	1.160937058	0.683006462
775.7	928.8	536.6	496.5	282.4	336.6	1340.1	819.2	559.4	263.7	268.5	250.6	0.417462639	0.682902018
769.6	1037.3	621.4	977.1	385.7	626.9	1904.7	1078.6	736.3	731.7	248.3	244.0	0.386591623	0.682649756
3608.7	2211.7	3749.7	962.9	3161.7	4882.6	2635.5	4537.4	3096.2	754.4	1300.9	1357.8	1.174811864	0.682379846
270.9	228.4	374.9	159.8	374.4	398.0	285.8	441.3	301.1	105.4	208.5	96.3	1.053417308	0.682164922
159.3	151.9	137.2	140.1	117.4	126.7	314.4	203.6	138.8	108.0	64.8	15.5	0.441425966	0.681431284
1004.1	899.9	749.9	1067.9	643.5	683.9	1963.3	1236.5	841.5	571.2	306.1	175.2	0.428632065	0.680587905
54.7	5.8	15.9	40.4	39.1	16.3	214.5	42.3	28.7	116.5	13.4	18.8	0.133787059	0.6791292
279.2	269.6	251.0	318.0	236.4	234.4	629.2	390.3	264.8	110.3	100.1	31.6	0.420772148	0.678297553
190.2	215.8	150.4	207.1	132.3	287.8	447.9	290.9	197.3	73.6	110.4	55.0	0.44042569	0.678032126
37.1	29.8	47.3	40.6	46.7	80.9	120.8	69.5	47.1	36.7	25.4	17.8	0.389624724	0.677218225
183.6	190.3	110.0	343.5	157.4	69.7	806.3	259.6	175.8	314.4	64.2	94.1	0.217976385	0.677055243
296.7	73.7	148.3	522.6	170.5	31.1	996.0	306.2	207.2	539.6	194.3	179.5	0.207981928	0.676607003
173.4	178.8	144.8	179.1	163.6	133.7	373.6	240.0	162.2	122.1	72.9	19.0	0.434289895	0.675972222
2652.3	1860.6	2101.1	1780.1	1520.7	3386.7	1982.4	3281.0	2216.9	886.2	928.5	689.0	1.118299368	0.675674989
167.7	308.7	140.4	92.2	74.4	132.1	530.5	225.9	152.6	132.9	62.5	83.6	0.287643429	0.675446363
1398.2	703.0	1207.0	537.2	711.8	991.5	697.7	1370.4	924.8	233.4	480.9	332.6	1.325436183	0.674807604
2102.2	1159.8	1295.6	985.3	1106.5	2121.2	1386.6	2167.1	1461.8	563.7	897.8	513.2	1.054194132	0.674526633
119.5	74.9	64.2	27.6	74.4	68.7	63.1	106.2	71.6	17.5	28.2	29.4	1.133555133	0.673728814
843.8	783.7	835.9	549.7	393.8	895.9	693.1	1066.1	717.1	80.7	387.1	199.6	1.034675131	0.672695095
127.6	95.9	87.2	73.6	66.1	107.9	315.2	138.4	93.1	80.2	29.2	22.6	0.295228124	0.67252096
310.9	49.5	112.3	235.9	113.2	103.1	639.0	229.3	154.2	362.6	118.0	98.2	0.241243857	0.672380703
218.4	325.4	234.7	276.7	213.0	145.2	549.4	350.9	235.6	97.7	48.2	61.2	0.428755172	0.671321364
128.4	85.4	84.6	65.6	61.1	88.6	209.1	127.6	85.6	23.2	59.8	23.8	0.409531554	0.671187415
676.6	613.2	664.3	434.3	449.5	440.5	517.9	814.2	546.4	112.0	125.6	117.0	1.055070673	0.67110467
2929.4	2095.8	3482.5	1618.2	2579.1	3517.7	2378.1	4034.0	2703.8	1031.9	1238.1	759.4	1.136941506	0.670255365
40.4	60.9	32.4	79.4	67.0	59.5	132.1	84.5	56.6	45.8	20.7	17.3	0.428398426	0.669505559
35.8	14.2	13.5	19.1	32.3	36.3	64.8	37.7	25.2	15.6	15.5	10.8	0.388648982	0.668080594
392.1	396.2	364.8	386.1	261.3	567.0	913.2	591.3	394.6	290.3	157.6	98.4	0.432069701	0.667292385
64.3	50.5	56.6	31.3	19.2	189.2	65.4	102.8	68.5	12.7	32.6	61.4	1.047335168	0.666374895
514.8	294.7	324.9	571.9	250.2	319.5	1013.9	569.8	379.3	505.4	103.9	131.0	0.374147647	0.665777403
755.5	562.3	578.3	591.4	494.8	878.4	613.9	968.3	643.5	171.3	354.7	143.8	1.048134875	0.664542582
2239.0	1719.2	1916.3	1218.6	1463.3	2057.9	1689.3	2664.3	1769.1	589.5	854.2	380.8	1.047208903	0.663983035

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.5514.1.A1_at, BQ602873, MAGI1	1090.5	1056.8	553.1	1862.7	1503.0	671.5	681.3	898.6	509.1	987.9
Ssc.29687.1.A1_at, CO944324, PTPRO	223.0	308.4	369.2	253.3	353.0	447.1	546.3	401.2	586.4	395.5
Ssc.22197.1.S1_at, CF789080	340.0	512.4	246.0	686.7	391.8	377.0	223.0	247.7	187.4	244.3
Ssc.21972.1.A1_at, CF788062, DGKG	1688.9	2060.6	1048.6	2488.6	2042.6	836.2	1065.7	1432.7	928.0	1404.3
Ssc.21848.1.S1_at, BI847197	3758.2	4371.0	2176.3	5039.9	5625.6	2320.4	1893.6	4046.3	1183.5	3899.6
Ssc.10911.2.S1_at, CK459913, ADRBK2	198.7	190.8	175.4	109.0	376.2	129.6	88.1	111.3	71.5	129.1
Ssc.973.1.A1_at, BQ604969, FAM149A	223.0	216.8	183.5	266.1	310.0	206.0	100.8	181.7	97.8	165.1
Ssc.10624.1.S1_at, CN158392, METTL7A	1248.7	1770.2	740.8	2217.5	2651.9	631.0	962.0	912.2	325.5	831.3
Ssc.28427.1.A1_at, CF179898, XG	290.1	229.6	275.0	350.9	227.0	82.6	127.8	157.1	256.6	148.0
Ssc.22305.1.A1_at, CK465094, DAPK1	338.4	298.5	595.3	423.4	360.4	178.8	140.2	245.4	150.9	239.1
Ssc.29749.1.A1_at, CO942872, AKAP7	109.0	195.2	82.5	135.0	188.6	111.3	39.5	50.0	56.5	113.8
Ssc.24649.1.A1_at, CN159165, CHURC1	123.4	93.1	80.8	91.3	130.5	86.0	72.3	66.4	35.1	70.1
Ssc.15565.1.S1_at, CA780996, LCP2	106.9	105.7	78.4	167.9	214.0	85.9	45.3	94.0	70.1	73.3
Ssc.23980.1.A1_at, CK454528, PHF20	25.6	34.3	47.9	38.8	48.8	87.8	73.2	40.1	48.1	49.3
Ssc.28997.1.S1_at, CA781087, KCNH1	327.3	540.2	268.3	1287.9	1577.7	615.9	340.9	718.4	322.5	527.1
Ssc.15932.1.S1_at, BF078387, ITGAV	425.6	892.2	564.7	720.5	1074.2	1981.1	1642.5	1276.0	1025.2	788.3
Ssc.24795.1.A1_at, CK465257, WDR76	81.4	80.4	80.2	176.6	117.9	36.1	53.6	43.5	32.9	144.5
Ssc.6564.1.S1_at, CO948886, RASL11A	1041.5	757.7	1423.5	2360.8	1387.3	1145.1	981.5	1134.7	357.8	936.5
Ssc.27341.2.A1_at, CF368496, SLMAP	103.3	119.7	130.5	35.2	130.0	178.2	198.2	89.8	183.8	144.3
Ssc.1484.1.S1_at, AW346678, SHKBP1	367.7	293.1	478.3	688.8	461.6	363.9	193.2	292.2	140.5	306.8
Ssc.12927.1.S1_at, CN165867, HIGD1A	3648.9	4056.9	5427.1	3090.4	2978.5	7027.4	7018.5	4167.0	9470.2	5953.0
Ssc.10988.1.S1_at, CO947173, ABLIM1	869.4	842.0	656.0	1343.6	1273.5	328.6	502.7	720.9	409.3	980.5
Ssc.4878.3.S1_a_at, AW435689, MFSD3	836.1	339.6	281.5	372.8	630.2	363.2	222.0	305.3	188.7	321.6
Ssc.13632.1.A1_at, BQ602956, SND1	87.2	105.1	53.2	256.7	141.1	65.6	55.6	70.4	31.1	67.7
Ssc.17765.1.S1_at, CK457647, ZMYM6	580.3	917.3	516.3	947.1	952.2	274.3	228.6	501.5	275.7	510.9
Ssc.9191.1.A1_at, BF709843, ABCB4	189.4	202.2	202.8	186.3	160.7	296.1	371.8	207.0	382.4	201.9
Ssc.24994.1.S1_at, AW435919, RSL1D1	1426.6	1105.4	1098.0	656.3	954.4	1466.3	1392.0	2120.1	1942.3	964.2
Ssc.7196.1.A1_at, BQ598164, ANKRD27	1967.4	2729.7	955.8	2836.4	2686.7	598.0	1231.1	1243.0	549.4	1361.3
Ssc.22090.1.A1_at, CF795099, HS3ST1	1070.6	1154.9	1307.2	1394.0	997.4	861.4	709.6	921.6	522.4	689.7
Ssc.15543.1.A1_at, CA781000	370.3	444.0	319.9	652.3	498.5	297.7	294.3	371.2	183.3	295.8
Ssc.5953.1.S1_at, CN165353, C14orf119	315.6	384.6	339.5	466.5	445.9	292.0	250.8	284.2	175.7	266.5
Ssc.13822.1.A1_at, BM190281, RTN4	686.0	519.1	523.6	401.9	450.0	858.4	654.9	754.2	1314.9	401.1
Ssc.9136.1.S1_at, BX918559, CCRN4L	255.3	266.6	246.5	170.5	164.9	604.1	451.0	237.8	389.4	205.1
Ssc.24888.1.S1_at, CK463311, TLK1	32.0	70.7	70.6	95.8	76.1	79.5	37.9	45.8	18.2	40.2
Ssc.22965.1.S1_at, BX671616, FBXL21	170.7	86.2	118.0	246.5	130.2	161.8	90.0	74.4	82.2	68.3
Ssc.31182.1.A1_at, CO942150	279.8	227.2	352.8	419.3	255.2	266.9	156.1	214.3	143.8	202.6
Ssc.10695.1.A1_at, CO950830, ACSS3	1653.4	1668.9	1259.0	2081.0	2487.0	822.6	981.4	1786.1	491.6	810.7
Ssc.30512.1.A1_at, CO993010, CA7	157.0	142.4	84.1	124.0	148.2	41.9	58.0	123.2	60.9	97.9
Ssc.248.1.S1_at, NM_214071.1, NPL	132.2	130.8	115.7	184.5	320.3	120.4	96.9	138.2	56.5	98.1
Ssc.29171.1.A1_at, CO951158	258.1	140.1	127.9	175.7	267.9	137.7	73.7	128.7	131.1	110.1
Ssc.25191.1.S1_at, CK465038, C16orf14	132.5	94.3	145.4	100.1	131.2	158.7	177.9	192.2	224.3	254.8
Ssc.21169.1.S1_at, BE032622	1602.0	2135.1	1271.0	2877.2	2326.8	876.9	919.1	1204.0	437.0	1285.6
Ssc.21178.1.S1_at, CN163142, RAB27B	59.2	41.2	63.0	112.4	154.1	85.5	41.6	29.6	36.5	59.0
Ssc.14490.1.S1_at, NM_214385.1, PTGR1	387.0	311.1	321.4	472.3	485.1	195.6	207.2	338.4	185.7	293.7
Ssc.10048.1.S1_at, BE234120, DNAJC25	534.0	496.3	561.0	839.0	547.8	792.4	813.6	1077.3	1517.2	724.9
Ssc.22224.1.A1_at, CF789046, KIF5C	546.8	837.5	587.1	1199.8	731.8	416.4	350.2	503.9	291.6	579.0
Ssc.11166.1.S1_at, BX670311, IGSF9	1339.0	1474.6	1380.2	1776.2	1543.4	943.2	833.5	1415.4	908.5	895.5
Ssc.4004.1.A1_at, CN158574, SYNE2	1437.0	1434.3	831.1	2730.0	2102.6	724.6	551.3	1341.3	406.3	1275.0
Ssc.18059.1.A1_a_at, CN162701, LRIG3	327.4	501.6	270.8	515.4	420.8	156.2	224.2	264.3	104.7	260.6
Ssc.18498.1.S1_at, BF198358, VSTM2L	65.9	90.2	80.4	86.8	92.7	53.5	52.6	52.9	26.9	74.6
Ssc.13556.1.A1_at, BQ602690	501.9	552.7	510.8	771.9	719.4	360.9	332.4	463.6	177.1	530.5
Ssc.18497.1.S1_at, CF179608, NEIL1	375.2	439.2	340.7	714.8	507.2	303.8	295.1	197.6	212.2	288.7
Ssc.31045.1.S1_at, BF199318	179.8	101.6	121.3	396.3	280.5	84.9	147.4	130.5	81.4	203.0
Ssc.19150.1.S1_s_at, BX923313, BID	781.4	661.6	766.3	379.9	496.2	817.8	1126.1	670.7	1243.3	802.9
Ssc.7099.1.S1_at, CN163776, RFK	909.2	1107.6	1012.1	858.5	753.1	2124.8	1074.0	978.7	1980.2	1093.2
Ssc.8309.1.A1_at, CF363963, HSD17B11	889.1	693.7	547.4	1083.3	1174.1	539.5	679.3	623.2	269.2	771.9
Ssc.16769.1.S1_at, CN160319, CTSZ	1677.0	1012.9	1770.1	1123.5	3213.4	1123.5	814.6	787.3	509.2	1353.4
Ssc.22527.1.A1_at, CK466721, PBX3	1676.0	1801.2	1596.7	3261.1	2150.6	1185.2	1429.7	1567.6	1060.6	1706.4
Ssc.27429.1.A1_at, CK463721, CPEB2	178.0	208.6	119.2	180.3	304.3	111.1	131.2	134.4	108.3	118.4
Ssc.3361.1.S1_at, CK467540, COMMD4	421.9	361.6	356.7	394.9	453.9	219.9	186.8	225.1	151.4	286.1
Ssc.3065.1.S1_at, BE231606, PCYT1A	77.9	100.6	72.9	56.2	68.6	198.3	210.9	79.8	311.3	84.5

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
641.3	804.8	380.9	451.8	489.6	217.1	1213.2	749.7	497.6	495.2	192.1	204.7	0.410134463	0.663727635
412.1	323.8	331.1	255.0	250.3	319.4	301.4	475.3	315.3	62.8	86.7	59.3	1.046132236	0.663335437
135.6	213.6	196.2	137.6	183.7	151.5	435.4	255.9	169.7	170.3	71.8	32.7	0.38977445	0.663201501
852.6	1355.4	525.0	620.9	778.1	375.4	1865.9	1133.4	751.2	537.6	273.0	342.2	0.402620418	0.662825648
1718.4	2697.8	1621.1	2033.2	1456.2	1070.8	4194.2	2668.7	1766.3	1328.3	1259.0	555.4	0.421117257	0.661844058
84.0	27.1	57.4	108.0	76.6	66.9	210.0	105.9	70.0	99.4	25.6	27.2	0.33330159	0.660876133
103.5	85.5	91.0	99.7	156.9	58.6	239.9	150.3	99.2	49.0	48.8	32.4	0.413540103	0.660101145
528.9	587.8	291.0	756.3	385.5	349.6	1725.8	732.4	483.2	758.2	260.1	174.3	0.279973191	0.659726015
80.4	138.6	120.9	85.8	135.1	50.0	274.5	154.4	101.8	50.9	63.9	35.3	0.370829083	0.659241031
160.6	56.1	86.7	276.2	111.9	63.4	403.2	190.9	125.8	116.5	49.0	82.8	0.312045304	0.659140123
46.3	26.4	35.6	79.0	64.8	41.3	142.1	74.2	48.9	49.2	35.5	19.5	0.344220752	0.658852061
39.9	41.8	30.1	48.0	17.9	82.5	103.8	66.0	43.4	21.8	18.8	21.9	0.417710139	0.65726988
84.4	20.9	38.2	82.3	34.8	30.1	134.6	73.7	48.5	55.2	18.6	27.7	0.360008917	0.657216495
49.8	34.3	33.4	32.9	34.9	49.5	39.1	59.7	39.1	9.7	20.0	8.2	1.001364722	0.655499721
528.7	89.5	160.1	731.4	311.3	162.4	800.3	505.0	330.6	595.1	172.2	251.3	0.413063761	0.654639311
535.5	510.6	554.9	966.6	1593.4	1110.7	735.4	1342.6	878.6	257.2	477.0	431.4	1.194681642	0.654404572
37.0	54.9	33.0	53.9	40.3	24.8	107.3	62.1	40.7	42.0	46.7	11.8	0.378844362	0.654378622
521.5	518.1	548.4	448.2	991.8	544.1	1394.2	911.1	595.4	605.1	322.7	197.5	0.427031331	0.653426552
163.3	101.9	81.6	85.6	89.1	101.0	103.7	158.9	103.8	39.9	43.4	30.3	1.000096395	0.653090772
168.1	226.5	216.9	94.9	103.8	205.9	457.9	259.3	169.4	149.2	90.5	57.8	0.369840577	0.653054142
5690.7	3854.9	4679.6	3116.5	3167.9	5839.5	3840.4	6727.2	4391.5	988.2	1927.0	1206.5	1.143516927	0.652798135
479.9	609.2	363.2	421.4	242.1	188.6	996.9	588.4	384.1	297.1	263.7	155.0	0.385260976	0.652730569
180.4	284.0	152.9	289.5	92.2	97.6	492.0	280.2	182.8	234.1	72.4	87.2	0.371446766	0.652365315
34.3	49.0	29.8	37.7	47.0	29.4	128.7	58.1	37.9	78.3	16.1	8.4	0.294315768	0.651974288
188.6	249.5	189.6	427.5	177.0	167.9	782.6	358.2	233.4	215.5	136.5	99.3	0.298157518	0.651451703
252.5	172.6	183.1	131.8	175.0	224.9	188.3	291.8	190.0	17.1	86.5	42.6	1.00904681	0.650984558
1672.3	771.3	1093.1	677.2	548.9	1394.7	1048.1	1577.0	1026.3	279.0	461.1	441.0	0.979115385	0.650769192
576.4	682.6	919.6	718.9	488.2	501.3	2235.2	996.6	647.8	793.5	389.7	162.6	0.289832379	0.650069573
822.9	401.5	405.4	234.1	234.8	791.1	1184.8	740.9	481.6	164.2	156.9	263.3	0.406503379	0.650030142
176.9	253.2	136.1	228.3	185.4	144.5	457.0	288.5	187.4	128.8	67.2	46.0	0.410065646	0.649656798
160.0	187.9	97.7	200.9	151.4	191.2	390.4	253.8	164.9	65.4	46.5	38.0	0.42223759	0.649424835
555.9	574.3	493.6	297.1	460.5	721.7	516.1	796.7	517.2	107.6	335.7	140.6	1.002060244	0.649156939
272.0	156.0	289.9	71.2	191.5	488.1	220.8	377.5	244.8	49.0	162.9	143.4	1.108821042	0.648467027
23.8	18.6	25.8	19.5	40.4	44.3	69.0	44.3	28.7	23.1	22.3	10.9	0.416183855	0.648315283
32.1	87.2	64.1	66.9	64.3	55.6	150.3	95.3	61.7	61.7	38.0	17.9	0.41045769	0.647157541
132.6	191.4	95.1	179.5	121.2	43.8	306.9	196.7	127.3	78.3	49.3	54.6	0.414738534	0.646877436
453.4	774.4	653.9	633.9	463.4	808.0	1829.9	978.5	631.2	468.5	485.2	149.7	0.344926206	0.645048102
52.7	73.4	43.2	55.9	38.8	31.4	131.1	76.4	49.2	28.9	33.2	14.9	0.375425754	0.644584097
105.9	38.5	38.8	85.4	58.2	67.5	176.7	102.0	65.7	84.4	30.7	26.6	0.37191096	0.644154741
48.5	101.5	52.3	113.6	31.9	100.9	193.9	116.3	74.8	65.5	25.9	34.5	0.385600357	0.643242158
184.3	120.7	116.6	102.9	99.6	152.1	120.7	201.6	129.4	22.3	38.2	32.7	1.071803369	0.641763402
691.5	719.4	438.5	764.7	710.1	308.6	2042.4	944.5	605.5	627.6	334.1	185.8	0.29644572	0.64103107
64.6	26.2	16.4	40.9	21.8	23.9	86.0	50.4	32.3	46.3	22.4	17.8	0.37566876	0.64036479
159.4	172.6	149.6	175.0	150.0	130.5	395.4	244.1	156.2	81.6	68.0	16.6	0.395020824	0.639780982
739.4	639.9	665.7	430.6	470.7	830.2	595.6	985.1	629.4	138.2	326.3	154.0	1.056741994	0.638949798
339.8	330.9	246.0	379.3	175.8	169.3	780.6	428.2	273.5	261.5	115.5	89.5	0.35039286	0.638729314
648.8	845.9	563.4	748.6	575.4	446.7	1502.7	999.2	638.1	172.5	236.0	142.6	0.42466349	0.638631466
676.5	603.5	425.0	839.5	386.7	350.8	1707.0	859.7	547.0	727.6	425.2	192.1	0.320445226	0.636268466
107.6	199.7	84.6	160.1	124.7	93.0	407.2	202.0	128.3	107.0	69.6	44.1	0.315037656	0.635066007
37.2	35.6	24.6	48.9	21.7	30.5	83.2	52.1	33.1	10.7	16.9	9.8	0.397636218	0.634996801
234.7	180.2	207.7	289.6	223.3	284.7	611.3	372.9	236.7	125.5	135.3	43.2	0.387182255	0.634754626
117.5	209.5	157.7	180.3	117.0	206.2	475.4	259.5	164.7	148.2	50.4	41.3	0.346430525	0.634731
78.0	102.4	70.8	119.4	48.6	73.4	215.9	129.4	82.1	122.5	50.1	25.1	0.380268643	0.634270705
878.9	491.9	614.7	428.7	476.6	656.5	617.1	932.2	591.2	174.7	241.1	165.5	0.958087552	0.634243764
1612.5	480.3	926.3	671.0	532.6	1293.2	928.1	1450.2	919.3	137.0	553.9	452.6	0.990536221	0.633932799
266.7	345.5	304.7	578.0	252.0	442.5	877.5	576.6	364.9	261.3	191.5	124.8	0.415830978	0.632825778
631.0	532.1	485.7	737.7	670.5	420.0	1759.4	917.6	579.5	877.9	326.6	120.4	0.329377394	0.631538797
969.2	1307.7	781.9	996.4	587.4	614.1	2097.1	1389.9	876.1	684.3	266.3	272.1	0.417771356	0.630345109
59.0	118.4	102.9	44.3	97.4	34.2	198.1	120.7	76.0	67.7	11.7	34.7	0.383851642	0.630040879
166.2	114.0	109.9	147.5	76.6	191.9	397.8	213.9	134.4	41.0	50.0	42.1	0.337732529	0.62821472
138.5	56.1	112.6	98.0	187.2	73.6	75.2	177.0	111.0	16.3	97.0	47.2	1.475279107	0.627260398

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.25099.1.S1_a_at, BX668463, SPCS3	1100.6	1178.1	980.2	615.5	1062.1	2078.3	1977.6	1026.5	1798.7	1323.9
Ssc.6995.1.A1_at, BF712245, ZBTB20	265.0	233.1	171.1	393.4	335.2	117.4	185.1	208.8	82.6	186.8
Ssc.17821.1.A1_at, CF179680, FAM135A	177.1	154.9	215.9	412.9	372.6	94.0	137.2	370.8	126.4	127.0
Ssc.30616.1.S1_at, CO948664, GPC1	170.3	147.4	132.3	189.9	151.7	73.4	79.5	105.5	85.6	180.8
Ssc.7245.1.A1_at, BQ598334, TMEM38B	295.6	381.4	447.3	204.2	122.4	494.8	600.6	192.1	728.4	311.1
Ssc.11335.1.A1_at, BI181829, NEK7	180.9	120.6	130.1	191.2	170.1	72.3	93.9	135.4	66.6	148.9
Ssc.12809.4.S1_a_at, BQ598177	1483.1	1358.6	1241.1	2168.5	1727.1	541.1	923.4	990.8	1181.3	982.1
Ssc.10909.1.A1_at, BF702883, KCNK1	39.2	37.1	28.0	19.5	30.7	39.9	52.9	38.5	65.0	61.9
Ssc.4895.1.S1_at, BF713434, FBXO25	647.5	514.7	643.2	674.2	798.2	413.1	486.8	286.8	238.5	564.5
Ssc.24276.1.S1_a_at, CK452400, CMPK1	510.7	536.6	554.5	272.8	565.4	933.5	1073.4	408.2	1044.7	536.9
Ssc.18022.2.S1_at, CF794267, SLC33A1	258.0	343.0	286.6	233.8	279.8	734.5	539.2	390.7	360.9	422.7
Ssc.1347.1.S1_at, CO943484, TMEM62	464.8	399.3	354.5	537.9	575.1	275.7	312.0	289.8	157.1	260.6
Ssc.26491.1.A1_at, CF360135, EHD1	174.8	231.4	262.2	165.5	154.0	342.6	296.4	261.3	329.1	289.3
Ssc.26155.1.A1_at, CN162532	351.6	339.2	511.6	224.2	236.6	515.2	636.8	382.7	670.1	531.4
Ssc.11526.1.S1_at, CK459482, MAN2B1	690.9	563.4	647.1	787.7	823.8	441.0	435.6	617.2	357.8	453.5
Ssc.17027.1.S1_at, BI343623	625.4	601.7	649.5	243.1	377.3	728.3	1047.9	625.9	1580.6	778.6
Ssc.25407.1.S1_at, BX916257, BIRC6	83.7	68.8	83.6	130.9	105.4	70.4	55.2	86.7	38.8	36.2
Ssc.18736.1.S1_at, AY550050.1, POLR1C	570.2	574.2	610.6	369.1	483.6	597.5	896.1	661.8	1189.0	633.7
Ssc.25441.2.S1_at, AJ653657, C12orf35	953.5	1239.7	861.5	955.4	1251.4	605.5	722.6	495.3	587.9	949.6
Ssc.816.1.S1_at, CF790758, LEPR	2820.4	3992.9	2825.9	3869.1	5390.7	2295.4	2564.5	2391.4	1813.3	3018.1
Ssc.455.1.S1_at, AF299325.1	494.0	461.4	332.5	823.1	1069.6	232.7	144.6	344.8	203.2	288.7
Ssc.19484.1.A1_at, CF362946	144.5	107.7	110.9	160.7	93.7	90.7	72.0	64.9	52.0	103.5
Ssc.26269.1.S1_at, BX922015	443.4	343.8	382.4	465.1	295.6	668.3	548.7	511.9	645.9	555.8
Ssc.10965.1.A1_at, BI403154	1035.4	1203.7	975.4	1990.8	2514.6	784.5	384.4	746.5	346.9	761.4
Ssc.13723.1.S1_at, CF792082, PDSS1	164.7	125.4	148.2	82.0	90.3	183.7	243.1	100.6	443.6	138.9
Ssc.23192.2.S1_a_at, BX666359, DCXR	311.3	255.5	211.4	298.2	368.4	135.4	97.2	366.4	71.4	224.0
Ssc.27185.1.S1_at, CN160739, USP30	302.9	482.0	178.9	625.5	232.2	252.5	113.3	184.2	116.1	310.5
Ssc.9388.1.A1_at, BF710406, RNF130	398.8	513.3	466.8	657.7	689.2	391.8	328.7	368.9	244.3	454.1
Ssc.30059.1.A1_at, CO949339, MXRA8	2908.9	3678.2	3271.3	5763.0	4435.6	2600.3	1162.6	4038.0	1643.3	3102.8
Ssc.15404.1.S1_at, CA779356, CENPH	126.9	200.8	122.6	160.9	114.0	83.0	72.3	129.0	56.5	136.0
Ssc.27151.1.S1_at, BI336094, CCDC80	3358.3	2796.5	2822.6	1355.6	2257.8	1822.2	910.6	2020.4	1120.5	1517.5
Ssc.29662.1.A1_at, CO943658, INHBA	53.4	24.0	54.1	17.1	31.8	50.1	53.1	92.5	69.8	24.3
Ssc.1018.1.S1_at, NM_214301.1, CAT	1581.0	1677.8	868.0	1814.7	1626.2	1150.3	643.2	1054.4	364.6	1082.4
Ssc.14360.1.A1_at, CK467752, HYI	1113.8	1175.4	1102.2	2123.2	1434.6	525.2	346.8	1261.0	199.4	805.9
Ssc.18528.1.S1_at, CB469543, MFSD1	110.5	134.0	90.5	194.0	154.3	79.2	81.7	121.6	72.5	97.6
Ssc.10884.1.A1_at, BF713431, IFI16	350.2	606.6	143.4	612.4	572.5	154.3	138.7	158.9	211.5	235.4
Ssc.24569.1.A1_at, CK460980, RRN3	52.1	68.1	39.1	45.3	47.3	56.5	65.1	51.0	123.5	94.2
Ssc.19798.2.A1_at, CF368143, C12orf23	99.3	209.4	78.4	52.8	193.8	326.7	334.6	80.8	148.3	214.6
Ssc.2591.1.S1_at, BI402085, KLC4	397.5	341.9	209.6	393.1	365.4	226.9	176.6	204.0	111.0	244.6
Ssc.639.1.A1_at, Z80109.1, GEM	1674.3	1438.3	2960.4	1703.5	1059.4	5371.4	3789.0	3856.2	3318.4	2706.3
Ssc.15518.1.A1_at, CA780512, BCL6	2036.4	2161.2	2135.0	3980.9	2807.0	1172.9	1749.2	2631.0	1299.0	1709.2
Ssc.18454.1.A1_at, CF360141, TLE1	907.7	1005.3	1155.4	1052.6	974.5	625.9	711.3	766.7	362.4	920.0
Ssc.15370.1.S1_at, BX666577, GMFG	386.3	295.1	217.2	491.7	509.9	269.1	153.4	363.5	177.7	244.1
Ssc.30619.1.A1_at, CO939530, MTFR1	585.6	373.4	549.9	325.3	324.3	611.0	700.3	488.8	1089.4	531.8
Ssc.13404.1.A1_at, CF791220, WDR75	653.6	657.3	590.3	358.1	389.1	719.5	1092.1	663.3	1072.8	638.1
Ssc.27840.1.A1_at, CO940986, VASP	1939.5	1330.9	1589.2	984.4	1220.5	2742.9	1954.5	1823.7	2344.5	2023.5
Ssc.6189.1.A1_at, BQ601447, SLC7A11	4062.2	2548.9	4709.2	2857.8	2424.8	4994.8	6739.1	5003.6	8041.8	2643.9
Ssc.8845.1.S1_at, BI182338, EMP1	4574.8	6277.7	5618.6	286.0	2205.5	11195.7	10843.8	2466.7	11122.3	4512.2
Ssc.16422.1.S1_at, CF793673, PLAA	504.6	616.1	483.9	234.4	358.9	673.3	707.1	425.5	1010.1	503.0
Ssc.4368.1.S1_at, BI817204, FBXO32	1096.1	470.1	1119.2	1411.2	978.3	858.1	398.9	991.4	178.6	752.1
Ssc.18640.1.S1_at, BX920140, UBE2D4	218.6	163.2	175.0	170.3	314.5	103.9	87.1	204.5	106.4	135.5
Ssc.11251.1.A1_at, BI181185, FOXO1	176.4	136.7	113.4	231.3	182.4	82.3	105.3	178.3	79.8	57.4
Ssc.1516.1.A1_at, CN159814, FARP1	492.2	416.2	437.5	479.2	639.0	295.9	279.2	329.3	356.8	339.0
Ssc.5079.1.A1_at, BQ605037, RASL11B	334.8	542.3	393.7	823.2	947.7	173.2	394.8	513.7	328.9	515.1
Ssc.13428.1.A1_at, BI404659, OTOA	251.4	169.1	204.5	292.6	243.7	203.5	119.1	124.3	91.8	125.5
Ssc.1882.1.S1_at, BX666107, FGFR2	633.9	929.1	373.2	1079.6	1343.7	650.9	403.0	608.9	378.4	716.6
Ssc.9834.1.A1_at, CF362626	430.5	453.0	437.9	647.4	1047.1	463.9	185.5	324.9	211.8	369.9
Ssc.11502.1.A1_at, BI183121, SDK1	192.1	190.8	155.6	259.9	213.4	73.5	150.2	123.6	174.6	95.4
Ssc.15231.1.S1_at, CA779027, C1orf123	434.4	383.6	446.0	579.9	432.1	282.6	217.0	434.2	207.5	371.0
Ssc.28175.1.A1_at, CN028591, TTLL5	170.4	165.8	113.0	203.3	186.2	74.2	72.8	117.5	46.3	98.9
Ssc.16839.1.S1_at, BG895518, DDAH1	1485.9	1364.5	1335.5	1081.9	1307.8	1821.8	1769.8	1920.4	2417.5	1938.5

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
1328.2	894.6	902.5	627.3	724.1	1689.7	987.3	1641.0	1027.7	219.7	449.3	403.6	1.040953442	0.626284786
84.8	177.7	91.0	113.9	88.6	30.7	279.6	156.1	97.8	86.9	53.5	47.8	0.349775838	0.626254216
146.5	73.7	109.7	84.7	69.4	157.9	266.7	171.1	107.0	118.0	112.8	37.9	0.401167442	0.625340971
61.3	91.6	79.0	58.3	48.3	55.2	158.3	105.0	65.6	22.3	44.1	16.3	0.414455954	0.625158791
421.5	178.8	273.8	261.4	173.8	435.5	290.2	465.4	290.8	130.9	216.1	114.4	1.002136605	0.624838848
49.8	88.6	64.1	72.2	53.7	58.7	158.6	103.4	64.5	31.4	37.1	14.2	0.406839871	0.623831625
485.8	679.9	649.5	650.7	640.5	346.0	1595.7	923.7	575.4	367.4	234.9	131.9	0.360598616	0.622902548
41.7	33.9	25.3	22.4	30.7	39.0	30.9	51.6	32.2	7.8	12.2	7.6	1.040992449	0.622902143
283.1	343.2	183.1	243.3	157.5	274.8	655.6	397.9	247.5	100.9	135.7	68.5	0.377539813	0.621953058
569.1	505.4	528.9	347.9	316.1	715.5	488.0	799.3	497.2	122.1	306.3	147.6	1.01875	0.621950609
375.2	251.6	234.0	151.1	241.8	571.6	280.2	489.6	304.2	40.7	152.7	149.4	1.085557617	0.621357571
119.6	202.5	173.6	175.7	147.0	146.3	466.3	259.0	160.8	92.1	60.0	29.1	0.344791845	0.620689211
275.9	164.4	187.2	157.4	162.3	183.8	197.6	303.7	188.5	46.8	32.5	44.5	0.954043932	0.620596563
404.2	259.8	369.1	252.1	290.2	462.0	332.6	547.2	339.6	115.6	113.4	85.4	1.020823312	0.62050776
359.9	298.7	250.2	272.4	327.8	207.0	702.6	461.0	286.0	105.5	95.1	54.9	0.407071081	0.620363542
894.2	538.3	701.5	326.5	410.0	672.8	499.4	952.3	590.6	179.9	384.3	208.0	1.182519023	0.62015626
12.2	77.8	23.8	30.2	40.2	29.6	94.5	57.5	35.6	24.2	21.4	22.6	0.377152131	0.620141548
600.9	375.3	548.6	352.9	421.3	661.0	521.5	795.6	493.3	97.1	249.1	127.7	0.94591658	0.620061503
428.6	514.4	427.7	531.8	321.4	276.0	1052.3	672.2	416.7	180.5	174.9	101.9	0.395942222	0.61984885
1386.4	2355.7	1233.8	1802.1	1051.6	1153.3	3779.8	2416.5	1497.2	1058.2	436.7	495.7	0.396092386	0.619542817
257.9	36.4	108.1	289.8	145.7	64.1	636.1	242.8	150.3	302.4	77.2	103.2	0.236328575	0.619165294
39.9	69.1	31.8	57.0	44.9	41.9	123.5	76.6	47.4	27.9	20.5	13.4	0.384075574	0.619072479
365.1	385.3	388.5	160.5	422.8	452.7	386.1	586.1	362.5	69.9	67.4	103.7	0.938930045	0.618445597
633.2	210.1	239.5	521.8	399.4	239.4	1544.0	604.7	373.9	678.1	219.1	174.8	0.242166349	0.618282237
187.0	107.3	137.9	71.8	117.6	201.1	122.1	222.0	137.1	35.8	134.8	49.2	1.122802708	0.617698291
89.3	180.3	104.8	123.9	79.7	84.4	289.0	178.9	110.4	59.2	119.7	37.9	0.382059801	0.617173524
62.0	200.4	95.2	166.9	97.7	100.5	364.3	195.3	120.5	185.5	86.1	52.0	0.330634093	0.616680319
233.4	258.3	185.6	237.8	178.6	227.8	545.2	357.6	220.3	124.5	77.9	31.4	0.404009832	0.615980535
1613.2	1893.6	1581.6	1412.1	1654.7	1113.9	4011.4	2509.4	1544.9	1131.6	1146.8	261.9	0.385114922	0.615625249
45.0	79.9	39.4	60.0	62.6	64.3	145.0	95.4	58.5	35.9	35.3	14.5	0.403566832	0.613814318
965.3	1323.6	648.0	1047.6	994.4	462.9	2518.2	1478.2	907.0	757.5	464.8	306.2	0.360170389	0.613544936
34.8	11.8	35.9	16.8	46.0	67.9	36.1	58.0	35.5	16.9	25.3	20.4	0.984848485	0.613066483
657.2	686.5	342.4	616.4	517.3	338.1	1513.5	859.0	526.3	371.4	340.6	155.1	0.347738855	0.612722842
332.1	467.2	291.0	496.9	545.2	171.1	1389.8	627.7	383.9	431.5	420.0	143.1	0.276230837	0.611663427
59.3	66.4	32.2	54.3	51.4	68.5	136.7	90.5	55.4	40.1	19.7	13.1	0.405019757	0.611467079
157.8	127.6	56.9	169.0	53.6	94.5	457.0	179.8	109.9	205.9	41.5	49.6	0.240470877	0.611370717
44.3	49.5	53.7	36.4	47.4	54.8	50.4	78.1	47.7	10.9	30.4	6.8	0.946473468	0.610854898
176.2	172.4	155.8	83.4	70.3	151.5	126.7	221.0	134.9	70.5	110.7	46.2	1.064646783	0.610558069
116.6	162.8	89.6	124.6	124.9	86.7	341.5	192.6	117.5	77.1	52.3	27.9	0.344167887	0.610182397
1996.9	2396.2	2012.9	805.3	4061.7	2662.3	1767.2	3808.3	2322.6	715.1	987.5	1063.0	1.314269061	0.6098717
1122.9	1339.3	1007.7	847.4	989.9	944.8	2624.1	1712.3	1042.0	817.5	571.7	171.0	0.397088526	0.608552439
624.0	447.4	363.7	424.1	311.5	301.6	1019.1	677.3	412.1	92.6	206.1	119.1	0.404327348	0.608407406
224.9	59.2	121.6	289.0	118.2	68.6	380.0	241.6	146.9	125.6	82.9	91.2	0.386582114	0.608199481
435.0	440.5	420.1	351.3	426.8	420.4	431.7	684.3	415.7	126.4	240.4	32.6	0.962898618	0.607493253
705.2	441.3	544.2	343.8	384.1	632.4	529.7	837.2	508.5	145.4	226.0	143.1	0.960013593	0.60741077
1834.0	1034.3	1464.1	952.4	1201.4	1445.0	1412.9	2177.8	1321.9	366.0	369.5	326.0	0.935569868	0.606967824
3898.4	3036.1	4294.3	1535.7	2927.4	4270.1	3320.6	5484.6	3327.0	1011.2	2040.5	1058.7	1.001933397	0.606603168
6795.8	2538.2	6198.2	1504.6	4008.1	8173.1	3792.5	8028.1	4869.7	2496.8	4207.9	2603.4	1.284018718	0.606574707
478.1	431.3	395.7	326.2	322.7	461.8	439.6	663.8	402.6	146.6	226.1	66.8	0.915950074	0.6065582
396.3	471.4	137.6	338.8	833.6	135.2	1015.0	635.8	385.5	343.8	337.1	258.7	0.379794019	0.606277458
82.5	80.8	83.5	84.2	72.4	60.1	208.3	127.5	77.3	63.2	46.4	9.4	0.370823733	0.605977408
75.9	69.8	70.2	65.1	43.2	40.7	168.0	100.6	60.8	45.4	46.6	15.0	0.361917797	0.604419267
178.8	154.8	199.1	231.7	193.1	203.0	492.8	320.0	193.4	87.3	31.8	25.7	0.392469191	0.604351539
202.0	337.9	199.3	308.3	253.7	93.6	608.3	385.1	232.5	267.7	142.8	87.9	0.382132799	0.603590037
86.9	72.7	76.6	83.4	42.1	118.7	232.3	132.8	80.1	47.2	41.8	24.7	0.344728609	0.602730101
297.9	405.2	327.3	411.6	360.8	187.8	871.9	551.6	331.8	378.9	152.0	83.1	0.380509997	0.601506031
283.7	133.9	150.8	315.8	149.5	87.9	603.2	311.2	186.9	264.0	114.7	90.9	0.309913017	0.600685518
42.6	122.5	60.9	82.0	83.9	52.8	202.4	123.5	74.1	38.3	40.7	28.7	0.366261448	0.600329391
175.8	181.5	169.0	190.7	169.7	202.7	455.2	302.5	181.6	73.7	98.4	13.1	0.398872291	0.600299764
43.0	62.0	56.1	39.3	50.0	44.7	167.7	81.9	49.2	34.0	27.2	8.6	0.293211717	0.600235945
1491.9	1171.2	1100.9	1196.2	1021.6	1124.3	1315.1	1973.6	1184.4	147.0	257.7	162.5	0.900564207	0.600096271

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.23810.3.A1_at, CK466275, NFIA	3301.2	4885.1	3861.0	6099.9	5392.0	3378.6	2117.0	4211.9	1567.6	3713.1
Ssc.19252.1.S1_at, CN165006, CMTM7	676.1	466.7	448.1	477.4	561.0	307.6	274.5	396.9	245.3	516.3
Ssc.5331.1.S1_at, BG608672, KSR2	1131.5	1606.0	2357.0	1975.0	2051.0	1914.0	1151.6	1313.0	581.7	795.2
Ssc.10089.1.S1_at, CK450505, ZC3H7A	183.4	284.3	101.8	228.2	138.6	386.3	340.3	253.4	381.2	211.9
Ssc.25550.1.S1_at, BX918583, LY96	796.8	640.0	670.7	1289.3	1459.0	581.4	546.5	521.8	343.2	674.7
Ssc.14477.1.S1_at, U83114.1, CILP	346.7	658.4	278.9	1576.8	509.2	113.6	82.6	450.9	433.6	407.4
Ssc.19271.2.S1_at, CF791003, GATAD2A	294.1	339.4	472.8	225.3	245.2	401.6	615.2	385.2	769.9	376.6
Ssc.18707.1.A1_at, CF359944, CTTNBP2	536.2	849.1	769.1	531.9	767.0	138.2	312.3	684.2	163.4	685.2
Ssc.3214.1.S1_at, CK457660, RNASET2	798.3	768.9	741.8	904.7	947.5	536.8	316.6	498.4	350.1	582.5
Ssc.7834.1.A1_at, BQ599559	515.8	208.6	425.9	367.2	254.9	697.7	748.0	1032.4	676.1	550.8
Ssc.11274.1.A1_at, BI181397, PLSCR2	138.0	41.3	55.9	155.5	161.0	59.4	47.8	119.2	61.4	76.4
Ssc.10965.2.S1_at, CB480465	343.8	339.1	289.0	644.4	613.9	226.3	134.1	320.4	121.7	229.3
Ssc.6374.1.A1_at, CK457299, ARHGAP5	629.7	893.5	811.2	763.9	771.6	1169.0	1263.8	868.2	1967.8	685.6
Ssc.19008.1.A1_at, CF366238, NAALADL2	544.3	788.8	510.9	1346.1	1205.3	344.5	427.8	921.7	226.1	707.7
Ssc.29638.1.A1_at, CO943458, BBS9	132.9	243.4	117.0	449.1	524.8	151.5	84.1	173.2	64.9	88.9
Ssc.5822.1.S1_at, BI401144, ALOX5AP	886.0	709.0	600.6	1886.2	1467.8	496.4	225.3	538.2	211.0	568.6
Ssc.7451.1.S1_at, BQ598771, RHOU	778.5	1084.8	917.2	548.5	945.8	1423.7	1308.5	735.8	1852.5	1316.5
Ssc.7824.1.A1_at, CK466112, SEC24A	1853.0	1660.9	965.5	1617.4	1570.4	1960.3	1821.5	2259.5	3009.4	2700.2
Ssc.7250.1.A1_at, CN166275, PPFIA2	168.7	196.1	143.6	287.1	289.4	141.7	124.6	169.0	55.5	140.3
Ssc.6579.1.S1_at, CF368239, DNTTIP2	548.2	683.9	625.4	201.4	426.4	1035.9	1145.9	449.0	957.6	590.7
Ssc.5618.2.S1_at, BF079082, RALGDS	144.6	152.3	297.9	53.7	291.6	238.5	634.4	119.9	418.3	346.2
Ssc.10588.1.A1_at, BX921052, IFI44L	1255.2	1810.2	1421.8	2542.1	2540.8	789.7	751.7	1460.2	683.3	1637.3
Ssc.12475.1.A1_at, CF364971, PSPH	76.3	92.6	117.1	80.0	51.1	100.3	442.2	127.9	560.4	83.3
Ssc.24336.1.S1_at, CK456588, GMPS	936.9	1149.0	976.0	884.4	863.2	1627.4	1795.1	1204.1	2182.5	1211.0
Ssc.23774.1.S1_at, BI336501, LCP1	89.6	88.0	52.8	139.5	118.9	51.9	31.2	47.9	47.9	33.6
Ssc.11440.1.A1_at, AW326367, RCOR3	398.0	342.4	257.2	527.7	528.6	205.4	229.3	310.2	148.3	351.0
Ssc.10115.3.S1_a_at, CN156408, TUBB2A	4579.5	3495.4	4672.8	1634.7	2120.3	5515.8	5208.2	3933.9	6353.5	4829.7
Ssc.28040.1.A1_at, CN032443, PARN	353.1	353.1	339.6	394.0	357.2	215.9	154.3	241.9	71.1	340.9
Ssc.6670.2.S1_at, AW507068, SLC39A6	448.7	723.0	671.8	252.2	343.9	1279.8	1297.6	694.6	1213.1	719.6
Ssc.30747.1.A1_at, BQ604638, ARCN1	111.2	196.8	147.6	101.4	215.2	330.0	229.2	118.7	377.0	202.8
Ssc.25051.1.S1_at, CK459787, SPOCK3	527.3	642.6	165.6	283.3	1338.7	327.7	418.5	222.8	66.4	302.6
Ssc.16774.1.A1_at, BI398985, DDAH1	163.7	151.2	190.3	136.5	122.7	333.2	229.2	78.0	723.7	370.2
Ssc.1118.2.S1_at, CF359378	167.7	244.8	217.5	206.8	447.1	131.4	164.8	213.2	135.6	204.1
Ssc.14291.1.A1_at, BQ601713, ARHGAP28	76.2	93.9	48.6	155.2	84.5	58.4	66.3	43.7	76.7	46.2
Ssc.24329.1.A1_at, CN166587, PLCG2	298.4	352.9	344.9	144.8	224.0	1031.2	129.8	259.0	564.8	242.2
Ssc.21382.1.A1_at, CK453637, DUSP5	252.4	329.3	460.5	280.4	230.0	435.3	836.0	469.4	768.9	320.1
Ssc.3590.1.A1_at, CN166109, FZD1	108.0	129.3	161.9	237.3	193.0	148.6	102.8	76.9	49.6	80.1
Ssc.24758.1.A1_at, CK466750, ESRRG	91.2	74.2	79.7	98.8	80.5	206.4	121.9	91.6	157.4	80.7
Ssc.18528.2.A1_at, CA778953, MFSD1	1181.6	1488.5	1246.4	1507.4	1893.9	1159.6	992.5	759.3	544.6	1134.9
Ssc.12900.1.A1_at, BI404122, C1QTNF2	1083.0	1223.2	879.3	1697.7	1392.9	673.8	560.7	1350.9	487.4	878.9
Ssc.6472.1.S1_at, BQ603115, SPOCK3	2008.7	2741.2	810.2	2238.3	5593.9	1360.8	1637.0	1463.4	243.4	1387.8
Ssc.21285.1.S1_at, CN154322, KCNH8	145.1	181.4	87.8	203.9	195.6	89.5	113.3	102.0	95.7	129.0
Ssc.1674.1.A1_at, CN156808, SLC2A14	1493.6	1234.8	1712.8	1028.7	1036.4	2736.8	1763.5	2145.8	3790.7	1067.9
Ssc.19150.1.S1_at, BX923313, BID	304.3	260.0	289.9	157.4	254.1	343.6	417.7	273.9	621.0	323.4
Ssc.2979.1.S1_at, NM_214408.1, PRDX6	2414.1	2180.4	3222.7	1957.1	1888.1	4394.4	4190.8	3055.4	3477.1	2708.2
Ssc.13834.1.S1_at, CN153597, RYR2	144.5	121.4	90.8	87.8	257.1	59.8	33.0	78.3	31.7	151.0
Ssc.1230.1.A1_at, AJ458065, ARHGDIB	1156.1	966.6	1042.3	1738.7	1531.5	795.5	471.3	1560.5	617.2	697.0
Ssc.24337.1.S1_at, CK456846, MAPK9	248.5	108.2	178.5	552.3	178.8	251.1	83.2	270.1	57.9	138.5
Ssc.6733.1.S1_at, BF704521, AMD1	1483.3	1388.9	1591.4	1456.6	885.5	2096.6	1964.2	2420.6	3243.7	1727.0
Ssc.13868.1.A1_at, BM189934, DAAM1	98.1	72.0	44.0	188.0	102.5	55.8	43.3	111.8	32.9	55.7
Ssc.7641.1.S1_at, CK466301, FAM69A	523.6	698.6	817.2	278.6	415.2	1350.3	1120.9	749.2	1302.4	829.3
Ssc.3321.1.A1_at, BF442411, ALDH18A1	2311.9	2604.5	2784.6	2497.9	2263.2	4325.3	3525.1	3814.3	3617.4	3688.7
Ssc.17340.1.S1_at, NM_214348.1, PSME3	388.2	453.9	518.1	293.6	260.1	794.5	785.7	513.3	612.0	465.1
Ssc.21227.1.S1_at, BM190672, DBN1	173.0	153.3	185.0	89.0	117.9	264.5	218.4	252.4	380.6	307.9
Ssc.1447.3.S1_at, AW315746, CGNL1	1252.9	1529.9	1169.5	1936.5	2720.7	1087.1	929.0	1193.4	695.2	1519.3
Ssc.12977.1.A1_at, BI404425, PDLIM4	2325.6	2507.2	2999.0	1133.0	1161.7	3946.6	2412.8	2029.9	3801.8	3976.3
Ssc.10549.1.A1_at, BF711497, BOC	146.3	120.1	74.6	206.6	142.3	61.2	68.1	80.3	50.2	165.3
Ssc.22256.1.S1_at, CF789644, ENTPD4	281.2	179.6	306.6	213.7	191.3	509.9	532.8	410.3	643.9	478.4
Ssc.13978.1.S1_at, CK462401, CCDC28A	292.9	412.3	213.3	468.9	372.3	99.8	185.3	200.8	123.9	162.4
Ssc.10493.1.A1_at, BF702283, LANCL1	385.4	473.2	371.0	805.9	626.5	397.4	201.2	307.9	125.8	476.0
Ssc.29120.1.A1_at, CO986760, AHCTF1P	177.4	170.6	156.1	149.4	150.9	282.3	248.7	141.3	330.0	216.1

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
1676.9	2776.1	1451.0	2085.7	1926.3	876.5	4707.8	2997.6	1798.8	1132.8	1112.7	638.8	0.382075432	0.600055377
257.9	145.6	272.2	218.3	182.4	176.5	525.9	348.1	208.8	94.5	109.9	49.5	0.397095551	0.599841051
601.3	707.1	725.0	507.8	1106.0	495.1	1824.1	1151.1	690.4	470.5	514.6	225.2	0.378478885	0.59975965
182.0	190.8	220.5	192.2	128.6	216.9	187.3	314.6	188.5	72.1	78.3	33.1	1.006621809	0.599135465
379.3	307.5	279.1	321.2	314.6	314.9	971.2	533.5	319.4	377.3	121.2	32.9	0.328919368	0.598727945
184.6	283.0	54.5	381.8	83.5	81.4	674.0	297.6	178.1	525.8	183.1	131.2	0.264292779	0.598526085
462.3	245.7	326.9	188.8	276.4	327.4	315.4	509.7	304.6	98.6	175.9	93.3	0.965827414	0.597573736
158.7	456.7	286.1	238.8	43.2	238.4	690.7	396.7	237.0	146.8	271.2	137.4	0.343125899	0.597447016
281.4	211.9	263.6	387.4	295.1	197.9	832.2	456.9	272.9	89.3	117.2	68.0	0.327890192	0.597275725
486.2	496.1	379.7	222.3	647.0	423.5	354.5	741.0	442.5	125.0	178.3	141.0	1.248213345	0.597121008
40.3	46.1	50.0	51.5	44.0	28.9	110.3	72.8	43.5	57.2	27.8	8.2	0.393933901	0.596741717
197.0	69.4	87.0	180.5	137.1	67.3	446.0	206.4	123.1	168.9	81.1	57.0	0.275872119	0.59628804
971.6	658.7	689.1	542.3	590.4	801.6	774.0	1190.9	709.0	95.6	492.1	156.4	0.915979741	0.595316069
408.4	465.1	219.8	263.1	255.6	261.4	879.1	525.6	312.2	380.9	283.8	99.4	0.355181933	0.594096456
71.5	22.3	24.1	204.3	57.5	20.9	293.4	112.5	66.8	185.2	47.0	70.6	0.227530898	0.593375992
287.8	257.9	228.7	351.1	213.5	113.1	1109.9	407.9	242.0	547.9	175.2	79.8	0.218048748	0.593323527
918.0	956.7	996.7	409.0	397.7	1044.3	855.0	1327.4	787.1	202.9	398.6	300.2	0.920588877	0.592938577
2010.5	1377.6	1297.9	882.2	1088.7	1703.9	1533.4	2350.2	1393.5	335.2	499.2	410.1	0.908719393	0.592919124
64.8	108.8	95.6	58.2	23.8	96.5	217.0	126.2	74.6	67.7	42.6	31.7	0.343887301	0.591163577
666.4	445.1	463.3	432.8	361.6	595.0	497.1	835.8	494.0	191.3	300.3	113.6	0.993910863	0.591076229
263.1	184.4	240.2	162.6	151.7	244.1	188.0	351.5	207.7	104.9	194.2	47.3	1.104581073	0.590915989
536.5	833.8	584.2	767.7	361.0	683.5	1914.0	1064.4	627.8	607.1	448.1	171.2	0.327992045	0.589778037
184.1	153.1	216.4	65.3	157.7	153.4	83.4	262.8	155.0	24.1	222.2	50.4	1.85806761	0.589757248
1207.8	847.5	962.4	830.1	640.2	1174.8	961.9	1604.0	943.8	113.6	414.2	218.1	0.981183075	0.588396653
27.9	19.9	20.2	36.3	23.7	22.0	97.8	42.5	25.0	33.1	9.4	6.3	0.255728314	0.588235294
120.2	193.7	114.1	223.7	140.6	85.8	410.8	248.8	146.4	118.3	81.5	52.2	0.356273431	0.588128918
4482.4	2193.2	3694.7	1731.0	2108.5	4008.1	3300.5	5168.2	3036.3	1389.7	889.6	1161.4	0.919945423	0.587497565
104.4	155.1	113.1	134.4	149.0	65.8	359.4	204.8	120.3	20.5	100.6	33.2	0.334724541	0.587344986
1007.0	529.0	520.6	388.0	395.0	827.9	487.9	1040.9	611.3	204.3	306.5	251.1	1.252766847	0.587209637
191.9	134.3	142.4	109.8	130.3	177.5	154.4	251.5	147.7	50.5	103.0	30.9	0.956358456	0.587182953
214.5	190.6	148.6	181.2	51.3	156.5	591.5	267.6	157.1	458.6	132.4	57.0	0.265624119	0.587132536
191.3	178.3	229.5	190.1	225.6	205.7	152.9	346.9	203.4	26.0	239.2	20.7	1.330564277	0.586451787
96.5	105.0	108.2	81.8	106.3	99.5	256.8	169.8	99.6	109.9	37.8	9.7	0.387685957	0.586208927
46.7	53.1	23.9	47.1	19.0	15.1	91.7	58.3	34.2	39.3	13.8	16.6	0.372491274	0.586165465
327.7	365.6	327.2	174.0	124.3	247.6	273.0	445.4	261.1	88.1	365.1	96.1	0.956288156	0.586139799
360.1	225.4	380.9	108.0	374.6	540.8	310.5	565.9	331.6	91.7	224.1	148.4	1.067993473	0.585986736
56.0	47.9	36.4	46.5	75.7	59.0	165.9	91.6	53.6	51.3	37.0	13.4	0.322985734	0.584970888
59.7	81.8	83.2	54.7	68.5	113.8	84.9	131.6	77.0	9.9	51.3	21.4	0.906573987	0.584726444
540.7	585.6	466.1	508.1	358.1	761.6	1463.6	918.2	536.7	280.4	262.5	134.7	0.366708574	0.58452591
409.7	717.7	429.3	458.1	466.9	290.1	1255.2	790.3	462.0	310.9	346.5	140.6	0.368036413	0.584516368
802.8	964.6	725.1	811.4	228.2	739.5	2678.5	1218.5	711.9	1777.4	555.6	251.8	0.265799502	0.584279868
67.2	59.2	71.6	62.7	57.2	53.2	162.8	105.9	61.9	47.6	15.6	6.8	0.380007373	0.584041549
1734.2	1024.8	1576.0	523.0	876.3	2325.7	1301.3	2300.9	1343.3	298.0	1029.9	657.9	1.032332765	0.583819367
315.7	171.0	235.9	198.0	181.5	284.1	253.1	395.9	231.0	57.4	136.0	58.6	0.912670196	0.583535394
2889.2	1641.2	2220.0	1223.5	1539.3	2968.7	2332.5	3565.2	2080.3	538.7	721.3	732.5	0.891890463	0.583509575
57.3	38.6	31.2	79.0	19.3	21.7	140.3	70.8	41.2	69.3	48.9	23.0	0.293495819	0.582014321
504.9	265.1	407.5	481.9	984.7	246.8	1287.0	828.3	481.8	333.0	426.2	268.8	0.374360289	0.581693428
111.9	21.1	66.2	70.8	232.8	55.8	253.3	160.2	93.1	174.4	96.4	74.4	0.367606412	0.581293706
1701.8	1521.9	1411.2	822.9	1200.9	1314.1	1361.1	2290.4	1328.8	275.7	588.9	301.9	0.976240504	0.580155605
47.0	32.8	26.0	27.7	51.7	23.3	100.9	59.9	34.8	54.0	30.5	11.8	0.344332144	0.580133556
893.3	633.2	650.7	520.9	377.8	649.8	546.6	1070.4	621.0	215.6	272.0	170.4	1.135939558	0.5800994
1946.8	2255.7	2201.5	2102.7	1584.7	3109.4	2492.4	3794.2	2200.1	213.9	315.1	506.4	0.88272977	0.57987363
511.6	275.9	400.8	233.4	218.5	562.1	382.8	634.1	367.1	107.7	151.9	147.2	0.958905899	0.578833659
133.6	162.9	225.7	122.8	176.9	166.4	143.6	284.8	164.7	39.7	62.4	36.3	1.146732572	0.578440324
686.5	814.3	523.6	739.1	398.2	595.2	1721.9	1084.8	626.2	633.6	306.9	151.8	0.363639003	0.577203171
2301.4	1917.9	2151.3	1487.3	1357.5	1981.0	2025.3	3233.5	1866.1	838.5	936.1	371.2	0.921377903	0.577107843
25.7	20.7	63.0	57.7	45.8	81.3	138.0	85.0	49.0	47.8	46.2	23.1	0.355365512	0.576727045
350.2	206.2	336.8	203.0	295.1	389.4	234.5	515.1	296.8	56.3	85.5	77.5	1.265708518	0.576211186
97.6	138.8	51.9	103.1	88.2	53.9	351.9	154.4	88.9	100.6	42.1	32.7	0.252647232	0.575735992
120.2	205.4	151.7	260.0	157.0	147.4	532.4	301.7	173.6	183.6	142.0	50.5	0.326101928	0.575537581
168.1	167.8	128.4	93.9	85.5	197.2	160.9	243.7	140.2	12.5	71.1	44.9	0.871146196	0.575139527

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.21604.1.A1_at, CO986989, NHP2L1	3510.1	3197.0	3814.9	3177.4	2590.8	4948.2	4749.2	5282.8	5665.1	3881.6
Ssc.4717.1.S1_at, CN161493, PHKB	538.7	582.0	372.5	563.6	617.5	381.4	313.3	343.2	263.5	426.6
Ssc.17233.1.A1_at, CF795667, PDE4D	341.8	330.5	119.5	305.0	308.3	97.7	113.4	95.6	113.3	153.4
Ssc.23853.1.A1_at, CK450644, NEK5	426.9	427.1	223.5	310.9	448.0	130.2	118.0	167.8	108.8	190.6
Ssc.29773.1.A1_at, CO946647, MAP2	950.4	930.4	791.3	1774.8	1036.5	627.2	518.6	946.1	432.2	833.3
Ssc.5772.1.A1_at, BI181334, IL27RA	327.3	208.8	644.7	227.6	156.3	606.8	511.6	380.2	438.8	516.1
Ssc.1856.1.A1_at, BE232628, ACAA2	265.1	216.2	224.9	309.7	314.2	199.9	132.6	144.7	85.0	212.0
Ssc.13271.1.S1_at, AJ747649, TRAM1	363.0	436.0	402.9	313.8	437.1	1118.4	781.5	570.0	768.7	536.5
Ssc.10147.2.A1_at, CO938490, BXDC1	130.4	100.2	97.5	75.7	36.0	116.2	165.3	176.4	236.5	120.5
Ssc.5962.2.S1_a_at, CK462554, MBD2	322.3	393.3	328.9	102.0	317.3	469.2	550.6	246.0	622.6	311.3
Ssc.5164.1.S1_at, BQ602181, TIPIN	361.9	432.3	386.0	344.6	445.4	509.7	862.8	404.1	922.7	296.1
Ssc.1271.3.S1_at, BP165107, FAM152A	227.0	259.9	242.1	50.4	279.6	342.1	547.4	92.5	431.7	237.1
Ssc.22622.1.S1_at, BX666099, SPAG9	855.4	1057.3	1041.2	349.1	658.2	1324.7	2518.3	768.9	2199.6	1182.3
Ssc.25792.1.S1_at, BX922492, PIGP	411.8	462.2	441.7	628.5	681.9	326.2	207.6	304.8	168.3	376.7
Ssc.11401.1.A1_a_at, BI182352, TEP1	651.6	629.0	529.0	345.8	728.4	343.2	297.1	263.4	223.4	310.3
Ssc.30827.3.S1_at, BP440001, TBC1D1	377.9	413.4	516.3	102.4	289.6	739.0	457.7	532.4	543.9	651.7
Ssc.24364.1.S1_at, CK452210	401.1	303.9	536.8	175.7	247.9	386.6	517.5	493.3	788.0	387.0
Ssc.30282.1.A1_at, CO989520, TNNI3K	177.9	299.7	151.1	324.6	313.4	131.9	120.5	145.6	55.8	128.9
Ssc.5154.1.A1_at, CF176179, LRRC17	229.3	158.1	223.0	218.2	257.5	208.5	101.7	123.6	72.0	181.8
Ssc.14193.1.S1_at, CO945481, KIAA1731	1011.9	881.4	762.9	796.8	774.6	1466.5	1683.0	1207.4	1996.6	1005.8
Ssc.26820.1.A1_at, CN160590, SLC39A10	630.7	486.8	743.0	677.5	495.9	948.4	1137.7	867.4	751.5	884.2
Ssc.18509.1.S1_at, CN154465, TMEM42	342.6	306.3	278.1	383.6	364.8	167.2	211.6	187.3	126.6	235.5
Ssc.3768.1.S1_at, BG732929, C11orf48	784.2	700.6	900.1	392.2	487.7	1148.6	1222.3	957.7	1441.2	779.2
Ssc.30124.1.A1_at, CO986859, HECW2	97.5	122.4	75.8	142.3	107.7	63.2	68.0	95.6	59.6	67.7
Ssc.8644.2.A1_at, CF180623, PDS5B	44.9	61.2	71.1	60.3	43.9	141.0	98.3	36.5	108.8	81.0
Ssc.10619.1.A1_at, BQ597410, ZNF677	148.1	109.2	95.5	113.0	138.2	62.7	75.7	81.4	87.3	90.1
Ssc.10226.1.A2_at, BI400884, RHOB	278.2	545.2	418.3	141.3	473.9	979.5	610.5	249.7	515.2	498.9
Ssc.30777.3.A1_at, CF360469, BBX	785.1	634.8	606.8	1344.3	829.4	403.5	483.4	765.7	267.0	845.1
Ssc.2991.1.S1_at, BI338583, PTPRM	169.2	165.4	198.7	176.2	97.2	287.0	236.7	280.5	186.3	234.8
Ssc.19271.3.S1_at, BP457326, GATAD2A	92.0	117.2	124.5	54.5	98.4	147.1	200.1	100.4	225.1	134.1
Ssc.6514.1.S1_at, BF194541, GALE	284.5	234.1	253.8	89.7	97.7	278.8	430.3	422.8	631.9	295.8
Ssc.12171.1.A1_at, BQ603723, FAM13A1	77.4	71.6	59.9	54.4	86.0	79.3	88.0	91.8	203.5	99.7
Ssc.8557.1.A1_at, CN153098, ST7L	525.1	651.0	317.0	690.4	654.5	299.4	292.2	336.4	146.8	392.3
Ssc.8169.1.A1_at, BI399193, MPPED2	356.5	634.7	491.0	1284.8	628.6	377.4	502.0	467.2	263.4	293.1
Ssc.27106.1.A1_at, CN166740, PTPRM	677.5	694.7	766.7	742.2	1100.4	286.7	464.9	601.6	755.2	481.5
Ssc.21937.2.A1_at, CN028149, USP10	175.8	161.8	159.8	142.2	141.9	168.6	191.5	242.3	339.9	238.5
Ssc.26563.1.A1_at, CN167070, TET2	39.7	46.3	47.0	45.1	35.0	27.8	19.6	35.4	28.9	19.9
Ssc.24303.1.S1_at, CK455135	207.5	262.5	167.0	174.2	259.8	323.1	284.0	442.4	344.3	258.7
Ssc.1703.2.A1_at, BI183996, HIST1H2BD	1232.6	1088.6	1371.7	261.4	1130.4	1433.9	1741.4	553.8	2182.8	2060.8
Ssc.2803.1.S1_at, BI342739, HINT2	1083.1	968.6	754.5	1069.7	1151.7	539.0	506.3	702.9	381.3	775.2
Ssc.12135.1.A1_at, BQ603671, CBFB	73.4	187.0	138.7	57.1	143.4	207.5	283.5	78.5	232.7	115.7
Ssc.3119.1.A1_at, BQ598786, C2orf30	1573.9	2135.9	1989.6	4189.6	2372.4	1866.4	1369.3	1875.4	862.1	1825.0
Ssc.29805.1.A1_at, CO947441	334.8	511.3	437.9	935.7	511.6	292.3	328.7	437.8	228.0	288.8
Ssc.18658.1.A1_at, CF360427	1743.2	1584.9	1491.2	2189.8	2507.0	757.0	1195.2	1570.1	1314.7	1329.4
Ssc.610.1.S1_at, CA778512, MAPK6	311.7	324.2	234.7	177.6	280.9	697.7	526.6	415.6	756.9	271.2
Ssc.30052.1.A1_at, CO949111, ZNF613	364.4	312.6	292.6	434.5	306.4	214.2	214.6	261.3	162.2	221.8
Ssc.28465.1.S1_at, CK464548, PGM5	2860.9	2958.8	1862.8	3821.6	3123.9	951.7	1235.0	1747.9	699.9	1723.9
Ssc.30428.1.A1_at, CO991781, MLLT3	139.8	93.2	74.1	136.2	84.7	41.7	71.5	153.2	30.1	36.5
Ssc.23804.1.S1_at, CK451781, SLC7A3	359.7	491.8	278.0	563.4	520.3	296.6	208.8	278.4	230.9	384.5
Ssc.16682.1.S1_at, CN159906, RRP1B	637.6	665.6	589.7	436.4	478.1	774.1	1004.3	648.4	1403.1	827.7
Ssc.31005.1.A1_at, CO986403, BAZ2B	283.6	211.1	154.3	160.9	320.2	138.9	112.6	166.4	133.0	137.6
Ssc.13212.1.A1_at, CF365390, PLEKHA6	769.9	987.3	637.5	910.3	591.6	298.8	158.6	464.6	212.6	527.6
Ssc.30602.1.A1_at, CO994988, ZC3H12D	64.2	49.7	37.5	69.0	60.7	29.3	28.8	28.5	33.1	27.8
Ssc.29707.1.A1_at, CO945204, MEGF10	108.0	100.0	53.1	75.2	72.5	53.3	37.1	82.8	37.5	49.6
Ssc.30446.1.A1_at, BI184974, BAZ1B	106.8	95.0	84.4	65.8	63.6	26.0	49.5	93.1	31.7	62.0
Ssc.5826.1.A1_at, CF367985, CSF1R	1149.4	915.4	747.2	1516.2	1694.6	499.2	316.5	685.0	446.3	580.7
Ssc.24545.1.S1_at, CK459904	199.7	219.1	158.5	141.6	152.3	317.9	316.4	137.0	349.0	232.3
Ssc.6631.2.A1_at, BQ599850, DMTF1	144.5	121.0	81.2	294.0	151.4	107.9	54.5	49.0	75.3	131.6
Ssc.26719.1.S1_at, CN160623, SURF6	801.4	704.5	1009.3	523.3	648.4	844.4	1211.4	852.0	1872.1	761.0
Ssc.4779.1.A1_at, BI183287, CPM	114.4	60.2	110.3	102.0	107.5	35.4	79.4	41.7	25.1	61.1
Ssc.15622.1.S1_at, BF189147	798.5	797.7	798.4	867.5	905.0	384.5	423.2	633.6	348.4	595.0

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
3501.4	2256.5	3092.0	2321.7	2291.5	3443.6	3258.0	4905.4	2817.8	455.3	669.7	595.4	0.864870699	0.574427126
178.7	282.1	159.9	209.9	166.9	193.2	534.9	345.6	198.5	95.2	62.5	44.8	0.371031672	0.57421875
119.2	41.4	42.4	115.6	34.9	41.3	281.0	114.7	65.8	91.6	23.2	40.1	0.234147036	0.573770492
54.8	137.0	92.9	82.0	68.0	57.8	367.3	143.1	82.1	96.8	34.8	30.5	0.223489799	0.573688379
363.0	516.5	314.1	446.9	485.8	180.8	1096.7	671.5	384.5	389.2	214.6	125.3	0.350618837	0.572640535
209.5	179.7	322.2	129.4	363.0	480.7	312.9	490.7	280.8	195.5	85.8	131.6	0.897136831	0.572141838
94.9	112.1	65.2	113.0	96.7	48.9	266.0	154.8	88.5	45.8	51.9	26.0	0.332556449	0.571342461
528.4	396.0	417.9	298.8	261.7	684.8	390.6	755.0	431.3	52.5	231.8	155.8	1.10422641	0.571198997
121.2	63.7	105.9	59.2	78.6	129.6	88.0	163.0	93.0	35.0	48.9	30.0	1.057677732	0.570826686
341.1	201.8	236.9	233.3	175.3	317.7	292.8	439.9	251.0	111.0	158.6	65.2	0.857414492	0.570570229
450.7	289.7	336.4	230.3	286.9	456.8	394.0	599.1	341.8	43.7	279.3	93.0	0.867424627	0.570541497
329.5	168.5	152.6	118.0	180.8	179.5	211.8	330.2	188.2	92.3	175.2	73.0	0.888338055	0.569875212
1651.4	854.6	1144.9	315.1	472.9	1027.4	792.2	1598.8	911.1	296.0	732.1	483.0	1.149967182	0.569847882
172.1	193.4	119.4	194.6	131.5	134.5	525.2	276.7	157.6	121.5	86.3	33.3	0.300033002	0.569468536
144.8	234.1	133.2	205.4	150.9	112.3	576.8	287.5	163.5	147.4	45.8	46.4	0.283393439	0.568561291
478.5	235.7	356.9	344.6	203.0	376.5	339.9	584.9	332.5	155.6	110.5	100.1	0.978269397	0.568491355
412.3	218.5	334.5	215.4	266.1	308.0	333.1	514.5	292.5	140.5	164.2	75.5	0.878067331	0.56847043
103.9	89.8	30.3	77.5	41.3	54.5	253.3	116.5	66.2	82.1	35.1	28.8	0.261374701	0.568188319
55.1	120.5	59.2	41.0	165.6	27.4	217.2	137.5	78.1	36.4	56.5	53.5	0.359696774	0.568159783
1046.7	840.1	876.6	566.3	798.1	889.4	845.5	1471.9	836.2	103.9	389.6	156.9	0.988977197	0.568124686
706.9	512.0	416.3	396.4	350.7	745.0	606.8	917.8	521.2	112.7	142.0	167.5	0.858987881	0.567873122
91.5	139.9	110.9	118.8	58.0	113.4	335.1	185.6	105.4	42.9	41.8	27.9	0.314601488	0.567855347
1119.1	446.7	683.0	372.8	336.2	821.3	653.0	1109.8	629.9	209.7	253.2	304.9	0.964607327	0.567534691
35.1	47.7	36.3	47.4	40.1	34.5	109.1	70.8	40.2	25.1	14.3	6.0	0.368181541	0.567400923
55.5	42.7	37.1	58.5	31.1	92.0	56.3	93.1	52.8	11.6	38.5	21.9	0.93846245	0.56718929
45.6	36.6	49.6	50.3	43.5	43.6	120.8	79.4	44.9	21.7	10.9	5.0	0.371412804	0.564786841
375.1	463.7	296.8	262.9	157.7	377.1	371.4	570.8	322.2	161.7	264.6	106.8	0.867619868	0.564539678
388.6	306.5	305.1	351.8	296.0	224.4	840.1	552.9	312.1	297.5	244.7	55.6	0.371472558	0.564377087
247.6	164.1	133.8	93.6	85.4	105.1	161.3	245.1	138.3	38.1	40.8	60.9	0.856989381	0.564215566
153.7	87.6	97.4	48.4	81.4	77.4	97.3	161.4	91.0	27.4	50.6	34.9	0.934888341	0.563853082
332.7	163.5	244.8	155.2	202.6	294.7	192.0	411.9	232.3	91.5	141.5	71.7	1.209887477	0.563823072
69.0	69.4	93.5	52.6	51.1	44.7	69.9	112.5	63.4	12.8	51.4	17.8	0.907290772	0.563607801
165.2	225.5	121.0	242.2	124.3	113.6	567.6	293.4	165.3	153.5	91.0	56.3	0.291226216	0.563356281
237.6	358.9	124.4	165.6	155.3	244.5	679.1	380.6	214.4	357.4	104.5	85.2	0.315678132	0.563247684
220.7	358.4	291.8	327.9	257.1	293.6	796.3	518.0	291.6	173.7	173.9	49.0	0.366172715	0.562923922
111.8	161.8	132.3	129.0	180.4	82.1	156.3	236.2	132.9	14.4	65.9	35.0	0.850287908	0.562754065
17.9	28.7	12.4	9.0	15.5	5.2	42.6	26.3	14.8	5.1	6.7	8.2	0.346863757	0.561676798
114.1	203.3	209.6	170.1	235.2	180.9	214.2	330.5	185.5	45.5	70.9	41.8	0.86616869	0.561371659
783.8	675.9	813.3	901.0	929.6	1267.1	1016.9	1594.5	895.1	436.2	650.8	203.3	0.880205977	0.56136357
302.7	376.8	329.6	437.9	300.1	209.3	1005.5	580.9	326.1	154.8	158.0	77.4	0.32427666	0.561274257
134.7	95.3	97.2	84.1	81.5	124.3	119.9	183.6	102.9	53.7	84.6	21.8	0.857655103	0.560246214
961.7	724.7	757.1	700.0	1018.1	1078.1	2452.3	1559.6	873.3	1013.7	443.6	165.1	0.356110776	0.559926222
171.7	254.4	161.5	181.4	129.2	160.1	546.3	315.1	176.4	229.4	77.5	42.1	0.32289264	0.559733858
747.7	878.4	638.8	749.4	737.4	389.7	1903.2	1233.3	690.2	431.1	299.0	165.8	0.362666078	0.559672851
351.6	304.0	275.4	208.2	192.5	459.4	265.8	533.6	298.5	60.2	199.8	98.7	1.123003035	0.55943903
111.8	126.7	108.8	138.8	88.8	144.7	342.1	214.8	119.9	58.4	35.3	20.9	0.350579753	0.558296869
696.7	1220.2	669.0	1038.0	313.6	317.5	2925.6	1271.7	709.2	703.0	464.2	369.0	0.242400419	0.557661257
21.5	68.9	30.5	46.8	38.8	16.3	105.6	66.6	37.1	30.4	50.9	19.1	0.351641414	0.557557558
184.2	137.6	107.9	163.7	76.2	263.1	442.6	279.8	155.5	119.4	68.3	65.3	0.351188325	0.555495998
639.2	520.2	481.7	354.3	437.7	667.6	561.5	931.5	516.8	100.0	293.0	119.7	0.920394909	0.554774276
74.7	105.5	78.7	85.9	65.2	47.8	226.0	137.7	76.3	73.8	19.2	19.4	0.337580745	0.554103123
193.8	347.2	114.9	266.3	135.0	48.0	779.3	332.4	184.2	170.2	159.1	108.8	0.236359904	0.554084948
23.2	5.4	18.9	12.2	12.6	25.7	56.2	29.5	16.3	12.6	2.1	7.6	0.290525317	0.553672316
28.3	51.8	9.9	34.3	25.8	22.4	81.8	52.1	28.8	22.2	18.6	13.9	0.351638943	0.552247407
19.1	45.0	23.5	22.5	45.0	18.7	83.1	52.5	29.0	18.6	26.8	12.6	0.34849214	0.55216673
469.2	91.2	126.3	616.5	305.7	64.5	1204.6	505.5	278.9	397.8	138.9	226.0	0.231536827	0.551687305
138.2	122.2	212.8	121.8	124.1	175.0	174.2	270.5	149.0	33.4	86.3	37.3	0.855237986	0.550852679
56.3	46.5	50.6	37.3	36.6	49.2	158.4	83.7	46.1	80.6	35.4	7.8	0.290893406	0.550840704
824.0	509.4	672.3	465.5	549.1	640.5	737.4	1108.2	610.1	182.3	461.0	130.6	0.827434068	0.55057241
42.9	17.0	18.0	39.6	27.5	15.3	98.9	48.5	26.7	22.1	21.7	12.1	0.270192826	0.550405164
313.8	307.8	159.8	249.2	260.2	284.2	833.4	476.9	262.5	50.0	128.9	56.4	0.314967243	0.550383696

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.10147.1.S1_at, CK456520, BXDC1	1432.4	1258.3	915.9	536.2	743.8	1057.7	1804.2	1134.0	2561.9	978.3
Ssc.3919.1.S1_at, CK452015, NT5C3L	1424.0	1284.5	1595.7	717.9	1083.7	1748.8	2024.1	1757.6	2674.1	1777.3
Ssc.16662.1.A1_at, CN159972, TMOD1	913.2	691.7	1167.9	733.9	724.0	1533.6	1406.9	1242.6	1515.8	778.3
Ssc.10800.2.A1_at, BQ598005, SLC25A14	171.4	161.4	129.2	192.9	145.3	85.7	78.3	104.1	113.2	113.9
Ssc.11430.1.A1_at, BQ604228, TCEB3	264.6	348.4	305.1	196.8	226.0	409.9	469.9	332.6	630.7	225.6
Ssc.25378.1.S1_at, BX915699, NMT2	101.7	103.0	118.9	81.3	100.0	99.4	202.3	191.2	364.3	141.6
Ssc.11689.1.A1_at, CK463849, CCDC41	519.1	465.9	383.3	694.7	1223.0	289.5	208.3	401.8	227.8	310.7
Ssc.1777.1.S1_at, BM190290, SNRPA1	1780.8	1682.8	1940.4	1132.4	1218.2	2487.2	3022.7	1951.1	3930.0	1848.3
Ssc.19304.2.S1_at, AJ746628, INHBA	308.1	138.2	842.1	158.6	181.4	565.8	590.7	1184.1	1064.5	116.0
Ssc.18337.1.A1_at, CF789283	206.0	205.7	174.7	332.1	385.6	172.0	122.5	149.2	62.6	197.2
Ssc.19271.1.S1_at, BI340315, GATAD2A	1054.1	929.7	1390.2	1037.9	745.6	1268.2	1903.8	1496.2	2243.4	1106.6
Ssc.19344.1.A1_at, CB480101, ARHGAP25	739.9	479.0	618.9	380.6	594.2	295.5	268.0	304.8	231.7	330.7
Ssc.3977.1.A1_at, BI181677, C16orf62	681.3	691.3	606.1	973.7	694.7	407.3	390.0	622.5	283.1	563.6
Ssc.5010.1.S1_at, CA779100, SNAPIN	855.7	1320.4	706.6	1462.2	1486.6	686.9	527.8	555.5	421.1	947.3
Ssc.13228.1.A1_at, BQ604874, PRKD3	35.2	41.3	28.5	15.2	26.5	39.6	69.3	35.1	69.4	39.9
Ssc.12911.1.A1_a_at, CF795801, SLC46A2	215.4	211.0	258.8	174.7	187.1	370.7	498.5	358.1	511.6	469.9
Ssc.8141.1.A1_at, BQ601038, MOSPD2	1991.5	2256.3	1269.0	1380.5	1804.2	1655.1	3589.0	1926.1	3259.1	2870.7
Ssc.11700.1.A1_at, CF793319	717.8	687.4	615.1	1204.1	977.6	532.6	509.5	417.5	313.5	733.5
Ssc.9551.1.S1_at, CN154581	438.4	645.4	454.1	692.1	935.1	431.2	278.8	412.7	233.1	648.4
Ssc.30692.1.A1_at, CO992498, RHOU	1020.5	921.1	1021.6	721.7	977.3	1500.0	1158.3	1033.7	2132.0	1548.0
Ssc.2142.1.S1_at, BF198653, C14orf124	496.9	369.8	402.8	236.8	288.0	447.7	604.8	554.3	697.7	553.4
Ssc.9766.2.S1_at, AJ679472, AK2	1049.2	1115.1	1216.2	716.0	1050.3	1428.8	1965.4	1138.8	2206.0	1376.8
Ssc.4857.2.S1_a_at, CK461143, PXMP2	177.5	240.6	170.0	221.8	244.4	180.4	93.0	127.5	70.7	193.4
Ssc.25182.1.A1_at, CK465762, GPHN	639.7	292.3	467.7	616.4	468.0	223.6	213.8	461.0	77.3	246.2
Ssc.9683.1.A1_at, CF363445	2547.4	3950.9	1741.5	2770.5	2686.9	2129.7	980.5	2489.4	1130.6	2286.8
Ssc.13430.1.A1_at, BI404701, MSR1	353.1	453.1	310.5	677.4	514.3	264.0	332.0	474.6	172.8	278.4
Ssc.6019.1.S1_at, NM_214196.1, DNASE2	344.6	271.0	350.3	378.0	757.8	211.8	132.2	321.8	182.1	189.9
Ssc.29076.1.A1_at, CO993813, PHKA1	205.6	262.7	200.1	349.2	210.5	208.8	119.5	169.3	89.3	172.5
Ssc.15164.2.S1_at, AW353854, DUSP28	668.9	505.2	593.8	555.6	702.6	335.9	329.6	375.0	342.0	423.1
Ssc.19354.1.S1_at, CF368378, CHCHD4	1099.8	841.5	1342.4	478.8	710.4	1312.0	1621.7	1247.5	2769.4	1126.9
Ssc.10593.2.A1_at, BF711776, IFI44L	209.1	172.5	181.5	233.9	306.7	94.1	115.1	208.4	71.8	133.3
Ssc.4673.1.A1_at, BM658769, C1orf56	667.2	495.8	892.3	609.4	382.0	814.8	731.0	838.4	1772.8	704.4
Ssc.9883.1.A1_at, BQ597604, ADRBK2	863.3	777.5	605.1	1089.1	1087.0	387.1	587.9	709.2	225.1	512.6
Ssc.1340.1.A1_at, BF709883, ATP13A3	1570.1	1392.5	1696.3	1259.4	916.6	2410.0	2671.4	2010.1	2623.7	1894.8
Ssc.833.1.S1_at, AY349424.1, C1QA	730.2	539.1	338.5	1393.5	1512.1	425.6	217.5	844.6	221.8	373.7
Ssc.30737.1.A1_s_at, CF789150, PNPT1	399.2	451.0	463.7	238.4	327.4	524.6	738.1	430.2	886.3	386.4
Ssc.14433.1.A1_at, BQ602282, ZNF274	113.6	122.5	63.0	216.8	208.4	99.5	53.9	82.3	53.4	81.5
Ssc.23994.1.A1_at, CK453077, PTGS2	663.9	2759.2	2275.9	598.8	657.8	2549.8	943.9	1858.5	4215.5	2236.9
Ssc.9698.1.A1_at, BQ603137	143.8	159.9	169.9	231.0	198.3	149.8	142.8	100.6	82.3	85.7
Ssc.8947.1.S1_at, BX667843, BHLHB2	203.3	298.2	318.7	89.1	275.1	469.6	413.4	193.9	401.3	344.5
Ssc.21926.1.S1_at, BX667248, LDLR	969.1	461.3	1565.6	250.9	343.7	1329.5	1555.1	716.8	1657.4	959.7
Ssc.14340.3.S1_at, AJ668033, LITAF	564.4	1034.3	783.1	149.9	1144.9	1419.6	2573.6	598.7	1189.7	746.6
Ssc.22130.1.S1_at, CK455807, EPHA4	337.2	582.5	263.4	711.3	942.3	179.6	559.3	438.1	263.1	260.8
Ssc.15544.1.A1_at, CA781015, TCTN2	452.5	326.2	237.2	634.4	443.4	287.9	200.9	238.9	159.2	363.1
Ssc.15701.1.S1_at, CK460093	1720.3	1544.5	1197.4	1625.8	1853.9	911.7	715.8	1300.2	785.5	1228.5
Ssc.18455.1.A1_at, BF080762, HIRIP3	302.9	220.9	233.3	274.1	227.8	180.2	132.8	176.1	169.4	176.7
Ssc.10695.2.S1_at, CK450664, ACSS3	1382.5	1643.0	946.6	2115.1	2395.2	822.1	921.5	1255.5	439.1	832.5
Ssc.16442.1.S1_at, CB288186, C10orf72	372.5	214.3	554.5	451.2	269.1	643.1	893.6	863.7	755.4	494.9
Ssc.26649.1.A1_at, CN153861, RAP1GDS1	128.0	53.6	66.0	128.1	126.6	37.7	66.4	89.4	31.6	80.7
Ssc.16686.1.A1_at, BI404742, FAM48A	871.1	822.4	484.9	876.1	1118.0	337.4	644.6	506.1	504.3	689.2
Ssc.21961.1.A1_at, BX667499, FBXO18	296.1	312.2	253.4	230.3	424.2	209.4	185.1	153.3	143.5	243.9
Ssc.19225.1.S1_at, CF366260, E2F3	886.1	871.8	1023.3	841.9	963.4	939.3	1623.2	1590.6	1829.5	1093.0
Ssc.21987.2.S1_at, BP164251, IFRD1	241.7	308.8	286.6	73.4	260.5	565.0	524.5	148.5	573.0	276.2
Ssc.2924.1.A1_at, BQ597908, RAB8A	139.8	63.6	108.3	143.7	140.9	59.3	55.1	105.2	63.6	102.7
Ssc.13068.1.A1_at, CF365867, PARP12	770.8	880.1	758.2	752.9	874.1	504.4	443.0	543.2	316.8	786.4
Ssc.13222.1.A1_at, BQ604850, C14orf104	82.9	95.3	104.2	105.3	68.8	110.6	138.3	144.4	158.5	175.6
Ssc.2893.1.S1_at, BI118371, CLN5	753.2	747.2	622.5	787.8	764.9	495.4	338.2	506.0	223.8	571.8
Ssc.460.1.S1_at, NM_214144.1, PRDX5	782.8	760.3	860.2	1193.8	1653.2	694.3	467.2	898.0	602.4	806.7
Ssc.18022.3.S1_at, AJ663333, SLC33A1	248.4	328.0	263.4	173.3	323.1	597.3	527.4	524.9	446.6	323.0
Ssc.4336.1.A1_at, BQ600981, SH3YL1	101.5	130.1	57.4	146.1	155.6	54.9	47.1	68.2	17.4	83.7
Ssc.18886.2.A1_at, CF365262, EP400	463.2	301.7	296.6	505.3	470.4	197.6	220.6	333.9	353.3	248.1

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
1472.6	534.9	918.7	446.5	476.3	1125.2	977.3	1507.2	829.0	367.1	674.8	416.5	0.848272146	0.550041356
1293.6	1169.3	1147.6	996.7	873.8	1093.3	1221.2	1996.4	1095.7	338.2	395.7	145.8	0.897275268	0.548851755
834.2	537.5	973.6	250.7	795.6	873.2	846.1	1295.4	710.8	199.6	311.4	268.2	0.84005011	0.54869388
77.7	65.0	37.5	45.3	45.0	54.6	160.0	99.0	54.2	24.4	16.2	14.9	0.338561193	0.547085353
336.6	181.0	301.4	127.3	162.2	249.4	268.2	413.7	226.3	60.6	151.8	82.8	0.843898377	0.547002143
152.8	74.5	106.8	63.4	77.8	178.6	101.0	199.8	109.0	13.4	100.8	46.9	1.079256618	0.545571352
280.0	36.4	125.2	290.5	133.9	75.5	657.2	287.6	156.9	336.2	76.6	105.5	0.23876547	0.545569386
1794.3	1167.0	1388.0	1199.4	1075.7	2031.1	1550.9	2647.9	1442.6	356.3	856.6	385.4	0.930146838	0.54481103
282.1	282.8	507.8	25.3	676.6	526.9	325.7	704.2	383.6	296.2	429.6	232.7	1.177792107	0.544692473
65.8	89.3	74.0	80.4	85.3	62.6	260.8	140.7	76.2	92.3	51.7	10.7	0.292283312	0.541814736
1306.5	727.1	910.0	398.9	785.3	1083.0	1031.5	1603.6	868.5	235.2	466.5	312.1	0.841945387	0.541559619
279.2	152.3	149.0	129.9	80.3	138.6	562.5	286.1	154.9	137.6	37.8	66.3	0.275338358	0.541285152
213.8	454.5	202.3	228.4	174.4	197.1	729.4	453.3	245.1	141.3	137.7	104.2	0.335997551	0.540664755
317.1	395.3	274.8	483.6	245.4	318.4	1166.3	627.7	339.1	361.1	202.2	87.0	0.290748521	0.54020901
16.5	39.7	30.3	12.1	38.7	26.9	29.3	50.7	27.4	9.8	17.2	11.3	0.932742559	0.540202658
259.6	162.7	162.2	106.4	280.1	460.2	209.4	441.8	238.5	32.3	72.3	126.8	1.139127666	0.539961367
2415.6	1425.2	1444.0	877.1	897.6	1550.4	1740.3	2660.0	1435.0	413.8	838.9	561.3	0.824560899	0.539467419
262.0	323.2	218.5	182.7	344.3	290.6	840.4	501.3	270.2	245.1	155.9	61.8	0.321533397	0.539010346
192.5	284.2	191.7	328.2	110.0	188.4	633.0	400.8	215.8	203.0	162.3	77.9	0.340958158	0.538452583
968.1	909.3	960.9	515.1	416.6	986.0	932.4	1474.4	792.7	124.8	428.0	256.3	0.850099381	0.537619823
427.4	259.0	272.6	259.1	302.0	322.3	358.9	571.6	307.1	101.3	90.8	64.1	0.855672593	0.537224302
1124.3	706.6	916.7	586.2	621.9	1267.1	1029.4	1623.2	870.5	187.9	444.4	280.5	0.845638714	0.536279028
68.2	81.4	55.5	90.1	62.0	70.5	210.9	133.0	71.3	35.0	53.4	12.7	0.338060008	0.535964912
148.0	170.3	107.4	109.4	153.1	97.5	496.8	244.4	131.0	139.8	138.0	29.9	0.263576346	0.535845814
825.9	1069.0	685.5	2068.6	495.9	650.2	2739.4	1803.4	965.9	791.2	696.5	573.6	0.352572059	0.535571698
159.1	184.4	105.3	171.8	218.0	139.1	461.7	304.4	163.0	144.9	111.1	38.7	0.352950095	0.535385727
178.7	69.4	53.7	186.6	91.5	86.7	420.3	207.6	111.1	192.8	70.2	57.1	0.264309844	0.535266911
92.7	142.8	63.1	80.3	51.2	56.9	245.6	151.9	81.2	63.1	47.3	33.9	0.33045626	0.534413133
205.6	294.7	231.3	148.9	156.9	120.1	605.2	361.1	192.9	80.8	38.8	64.1	0.318754613	0.534217619
1281.1	691.0	928.1	494.4	518.4	1265.0	894.6	1615.5	863.0	336.3	670.4	353.5	0.964698518	0.534199938
40.6	91.2	79.0	79.9	52.6	55.7	220.7	124.5	66.5	53.8	52.2	19.6	0.3012594	0.533964991
667.2	380.2	611.2	223.1	501.6	727.4	609.3	972.3	518.5	192.3	451.0	190.3	0.850838612	0.533231168
302.1	390.1	234.4	198.6	301.2	123.0	884.4	484.4	258.2	207.9	186.2	93.4	0.291987035	0.533121379
1647.4	946.3	1249.3	680.0	1100.6	1787.9	1367.0	2322.0	1235.3	302.0	353.8	420.8	0.903634289	0.531976744
250.2	47.1	116.3	656.0	174.5	85.4	902.7	416.6	221.6	522.6	256.3	224.4	0.24547274	0.531834037
452.7	263.3	379.7	187.7	215.2	393.6	375.9	593.1	315.4	93.7	212.7	107.9	0.838874998	0.53170803
16.4	64.8	28.0	74.4	27.0	25.8	144.9	74.1	39.4	65.9	20.0	23.9	0.271986746	0.531570426
844.6	798.9	1170.2	320.9	1127.2	3264.6	1391.1	2360.9	1254.4	1042.7	1199.1	1030.6	0.901719478	0.5313183
86.9	54.2	43.1	72.3	54.1	47.1	180.6	112.2	59.6	34.5	31.9	16.7	0.33013992	0.531153481
163.6	277.7	155.7	81.8	109.4	373.1	236.9	364.5	193.6	93.4	105.2	110.7	0.817080378	0.530943106
1026.0	321.0	880.6	138.7	463.8	1129.3	718.1	1243.7	659.9	549.0	398.0	406.9	0.918927199	0.530594195
1385.6	622.4	761.1	452.8	471.1	463.4	735.3	1305.6	692.7	397.3	782.1	360.3	0.942084172	0.530569938
201.1	215.7	170.2	267.1	129.0	97.7	567.3	340.2	180.1	277.0	154.6	61.3	0.317505082	0.529523586
121.2	196.4	97.7	147.1	99.6	131.4	418.7	250.0	132.2	149.8	79.1	36.7	0.315788636	0.528933333
549.1	608.5	382.0	821.3	369.8	405.6	1588.4	988.3	522.7	247.0	262.8	175.6	0.329087918	0.528883448
88.0	144.0	84.4	82.6	55.8	75.1	251.8	167.0	88.3	35.3	19.5	29.6	0.350741329	0.528715677
330.5	650.6	377.2	448.5	381.5	520.1	1696.5	854.1	451.4	576.0	291.3	117.8	0.266080355	0.528484792
383.6	414.1	337.4	260.9	728.6	190.4	372.3	730.1	385.8	137.0	164.4	186.8	1.036294943	0.528437469
35.9	41.6	24.9	52.3	27.1	12.1	100.5	61.2	32.3	37.4	25.6	14.1	0.321686907	0.528395465
276.0	276.3	293.5	258.9	224.2	367.8	834.5	536.3	282.8	226.8	138.4	47.8	0.338865588	0.52726606
68.2	96.9	137.7	102.6	87.0	98.6	303.2	187.0	98.5	75.1	41.1	22.8	0.324825221	0.526625321
740.5	737.4	831.0	687.6	732.3	741.7	917.3	1415.1	745.1	74.3	379.5	46.8	0.812256986	0.526516008
324.9	130.6	194.3	80.4	105.0	483.5	234.2	417.4	219.8	93.4	193.5	156.1	0.938442926	0.526502811
38.1	36.9	36.9	56.0	32.5	43.4	119.3	77.2	40.6	34.3	24.6	8.3	0.340712169	0.526474907
296.7	318.6	264.4	289.8	169.3	299.8	807.2	518.8	273.1	64.2	172.5	53.8	0.338321647	0.526447683
115.1	69.2	76.7	81.1	68.7	48.4	91.3	145.5	76.5	15.5	24.2	22.0	0.838262139	0.526074604
229.5	228.2	182.4	265.5	220.7	220.7	735.1	427.0	224.5	64.8	142.4	26.5	0.305392317	0.525711877
468.5	298.2	363.7	409.3	178.7	469.3	1050.1	693.7	364.6	379.4	168.9	112.0	0.347234126	0.525596302
368.7	209.2	228.6	137.0	162.5	418.4	267.2	483.8	254.1	63.3	104.5	113.9	0.950705982	0.525104718
24.5	62.7	23.5	24.3	24.2	11.4	118.1	54.3	28.4	39.7	24.9	17.5	0.240674905	0.52402015
174.4	99.5	190.1	151.4	113.1	121.7	407.4	270.7	141.7	100.1	69.2	36.1	0.347781268	0.523457702

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.18637.1.A1_at, CN162624, TTC33	115.3	163.8	151.6	148.3	157.2	89.0	112.4	63.5	63.4	113.7
Ssc.29281.1.A1_at, CO953055, SLC7A11	1494.1	789.9	2153.2	720.1	611.5	2352.4	2698.6	1472.1	4089.5	733.1
Ssc.4196.1.A1_at, CK465018, ZBTB44	1782.3	1951.2	1601.6	3096.5	1870.4	1270.1	1426.0	1780.1	1014.0	1236.9
Ssc.30288.1.A1_at, CO989873, GRHL3	129.9	118.5	78.7	49.6	172.9	57.9	77.7	40.9	41.8	88.9
Ssc.24384.1.S1_at, CK452203, TRIM41	420.2	459.1	390.8	782.1	622.7	238.7	295.9	418.9	215.5	382.0
Ssc.24937.1.S1_at, CK459809, C19orf15	357.1	289.0	386.5	251.0	213.5	561.0	603.0	311.7	1030.6	346.5
Ssc.24907.1.S1_at, CK459823, RAB8A	232.0	154.2	217.4	282.0	305.2	191.6	107.4	140.0	112.2	185.6
Ssc.26506.1.A1_at, CN070273, FBXL3	114.8	120.0	78.5	143.6	86.3	56.3	62.0	89.8	27.1	80.2
Ssc.14145.1.A1_at, BQ600501, SNRK	142.2	101.9	43.3	85.1	69.1	118.0	69.9	131.1	336.6	76.3
Ssc.22731.1.S1_at, BX666622, SEC14L2	248.6	224.4	293.2	162.4	229.4	386.4	322.0	397.1	394.7	267.9
Ssc.11367.1.S1_at, CF180782, VPS41	1068.4	1095.6	932.0	1092.1	1478.0	812.6	612.7	944.9	479.0	870.9
Ssc.1922.1.S1_at, BG835553, TP53I11	444.8	310.3	406.5	534.0	517.5	709.3	633.6	936.6	1144.2	558.2
Ssc.8697.1.A1_at, BF704189, TSC22D1	470.8	540.4	441.2	597.0	465.4	374.3	107.5	232.1	88.5	250.7
Ssc.19177.1.S1_at, BE232891, RCC2	338.0	558.2	429.2	217.8	355.2	700.8	622.0	350.8	734.4	481.9
Ssc.4849.1.A1_at, CF177468, GRIK2	1282.6	1047.8	1532.1	1323.7	748.2	1819.6	1644.2	1787.6	2340.6	1500.9
Ssc.19839.1.S1_at, CB477325, PSAT1	180.7	434.2	179.7	302.7	263.1	214.3	635.6	419.8	825.0	121.7
Ssc.2022.1.S1_at, BE235292, GPSM2	175.9	178.7	193.9	203.6	214.1	128.1	100.3	131.7	118.5	123.0
Ssc.13423.1.A1_at, BI404586, SFRS15	100.2	108.7	110.0	119.7	105.4	221.1	165.1	154.4	165.9	181.2
Ssc.29834.1.A1_at, CO951216, ZNF624	64.6	92.6	65.2	89.3	111.1	66.2	76.2	33.3	33.9	45.9
Ssc.16556.1.S1_at, CK467710, PRMT1	3376.9	2637.7	3638.8	1943.4	1923.1	3971.9	4296.7	4143.5	5347.2	3245.9
Ssc.7697.1.A1_at, CK451279, EFNA5	95.6	145.7	102.2	178.5	235.3	51.2	85.9	181.0	57.5	82.7
Ssc.6163.1.A1_at, CD572724, ETS2	631.2	921.6	779.7	1179.0	614.8	1623.2	1670.0	991.4	1779.5	1211.9
Ssc.22089.2.S1_at, CF787929, TAF1B	199.9	187.1	174.1	155.4	134.1	387.3	343.0	168.3	333.0	164.1
Ssc.22719.1.S1_at, CO952385, TIMM8A	1046.7	1051.3	1255.4	686.2	701.7	1197.6	1537.2	1232.1	2823.1	1215.3
Ssc.21554.1.A1_at, CA513716, VKORC1L1	1188.2	1026.2	597.5	920.0	759.1	590.1	2231.9	1482.6	1199.0	1320.5
Ssc.30145.1.A1_at, CO987122, SLC22A15	163.1	176.0	141.9	140.8	173.9	94.8	95.2	106.9	79.1	120.0
Ssc.2624.1.S1_at, BF080491	1076.5	1125.6	1137.3	1558.4	1735.1	808.5	844.6	877.3	677.9	1109.5
Ssc.27727.1.S1_at, BG895597, PGM5	5126.8	5295.2	3442.9	7027.3	6285.5	1854.9	2286.9	3369.3	1495.8	3490.8
Ssc.1118.1.A1_at, CF179500	1046.3	1325.1	932.9	2213.0	1707.7	799.2	1006.1	902.7	913.3	1034.4
Ssc.27656.1.S1_at, AJ662907, TM4SF19	344.3	421.2	250.8	296.0	317.9	233.8	188.9	230.3	144.9	288.3
Ssc.12583.1.S1_at, CK449898, JMJD3	247.7	151.8	227.3	275.1	188.3	223.9	344.8	345.0	556.1	185.1
Ssc.29366.1.A1_at, CO954416, TOP1	127.2	95.3	54.7	164.1	99.8	49.3	52.0	70.3	57.5	31.1
Ssc.1289.1.S1_at, CK454805, HMGA1	717.5	225.5	677.9	190.3	219.3	600.3	1244.8	805.2	1546.5	597.3
Ssc.4427.1.A1_at, BQ598146, TNIK	1474.3	1916.5	1144.0	2368.7	2138.8	1076.4	851.1	1390.8	333.6	1811.3
Ssc.7106.1.S1_at, CN159266, CDO1	1953.7	1815.4	3352.8	3388.6	917.2	1945.6	1164.6	842.2	438.6	1755.0
Ssc.21817.1.S1_at, CK451904, C6orf35	204.0	171.9	171.1	157.1	239.1	122.6	116.7	151.1	93.0	124.7
Ssc.30458.1.A1_at, CO992021, TIAM2	313.6	184.8	254.1	458.5	333.9	108.0	88.5	293.6	109.5	171.2
Ssc.2425.1.S1_at, BX926350, TJP1	2718.8	3453.8	2763.2	4875.0	2466.4	2413.6	2429.7	2354.0	1178.7	2139.8
Ssc.29136.1.S1_at, CN160286, GPATCH4	574.4	296.8	560.7	248.7	303.7	462.9	663.3	840.2	931.2	395.0
Ssc.14561.1.S1_at, NM_213908.1, ITGB2	255.1	245.1	174.4	353.7	561.0	83.5	122.5	180.7	118.5	124.8
Ssc.10776.1.A1_at, BQ597944, ZC3H12D	318.5	185.1	346.7	265.8	104.5	552.4	263.0	971.9	396.5	261.4
Ssc.4584.1.S1_at, BF440632, GFOD2	663.1	500.3	847.0	321.1	335.5	905.5	886.8	627.5	1399.6	669.8
Ssc.6078.1.A1_at, BI398893, STX17	250.0	302.6	227.2	423.1	317.9	298.7	116.5	248.1	89.7	254.7
Ssc.21910.1.S1_at, BX666465, C16orf84	311.0	267.1	347.0	165.7	267.1	373.1	434.0	322.4	683.6	324.4
Ssc.2185.1.A1_at, CO946931, ANKZF1	255.8	262.7	205.5	458.3	291.1	182.7	142.5	226.5	122.5	216.8
Ssc.10678.1.A1_at, BQ597644, RSBN1L	310.0	225.5	245.0	406.2	288.3	158.3	167.1	258.0	166.7	225.1
Ssc.30532.1.A1_at, CO993367, XRCC2	210.1	382.7	230.9	344.8	354.4	93.0	79.7	299.5	94.1	120.1
Ssc.30733.1.A1_at, CO993873, MKL2	3981.5	4226.1	2249.1	5665.6	5049.7	1215.4	3182.0	3009.4	2035.2	2661.1
Ssc.6139.1.S1_a_at, CF360612, WARS	1133.4	1430.9	809.1	635.7	914.1	1967.2	1076.3	1276.5	2379.5	1311.0
Ssc.24035.2.A1_at, CO954588, EIF2C2	2008.6	1491.2	2359.4	1457.0	1439.3	2177.1	3280.6	2446.8	3947.7	2155.5
Ssc.30580.1.A1_at, CO994268, ABCA13	120.3	207.1	83.6	267.8	387.4	44.9	37.9	66.9	38.5	89.3
Ssc.13009.1.A1_at, BI404548, IFITM1	7377.1	6555.8	501.1	9118.1	6676.2	646.7	639.1	8222.4	782.4	7333.9
Ssc.10611.1.A1_at, BQ597380, SMEK1	108.2	98.7	62.5	123.7	133.1	27.0	30.5	54.2	42.8	17.2
Ssc.4835.1.S1_at, AW668769, SKAP1	860.5	688.3	981.5	574.2	523.7	1078.4	1250.0	1105.6	1808.7	810.8
Ssc.24452.1.S1_at, CK457205, C5orf41	803.0	481.8	305.5	479.6	602.5	240.2	581.5	210.4	193.6	249.1
Ssc.23789.1.S1_at, CK460467, PRKAB2	111.8	118.8	77.4	64.9	159.4	261.8	111.2	126.4	189.5	111.7
Ssc.8209.1.A1_at, BQ601215, STRN	168.4	213.1	255.3	159.4	132.5	304.3	278.3	255.8	822.6	306.0
Ssc.12540.2.A1_at, CK450963, KIAA0182	339.7	310.1	313.7	229.0	205.2	454.3	551.4	406.1	501.2	476.3
Ssc.4756.2.S1_at, CF177248, ADORA3	69.4	93.6	82.0	91.2	284.7	106.1	92.3	94.9	48.7	59.7
Ssc.16511.1.A1_at, CK463681, CACHD1	620.6	698.3	855.0	1749.0	1491.7	676.3	645.1	783.4	292.9	788.5
Ssc.11054.1.S1_at, CN162874, POLD4	624.4	449.5	722.4	956.1	837.9	576.2	345.7	703.4	217.9	453.9

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
73.6	46.1	37.1	34.9	33.8	52.0	147.2	88.4	46.3	18.8	24.8	15.2	0.314113013	0.523190045
1056.4	1313.7	2004.7	262.1	1303.5	1181.4	1153.8	2269.1	1187.0	657.5	1274.7	560.5	1.02878126	0.52309098
791.1	881.3	583.1	707.8	709.1	545.0	2060.4	1345.4	702.9	593.6	284.0	125.7	0.34114735	0.52243909
21.2	43.1	17.5	63.2	24.1	23.4	109.9	61.4	32.1	47.6	21.4	17.7	0.291878942	0.52218967
152.9	204.5	143.4	180.4	133.7	156.1	535.0	310.2	161.8	164.7	88.4	26.1	0.30250352	0.521706426
299.2	330.4	314.8	127.2	207.8	506.5	299.4	570.6	297.7	72.0	287.2	128.2	0.994088571	0.521680454
65.5	63.8	73.1	103.7	83.3	71.8	238.2	147.4	76.9	59.0	39.7	14.8	0.322752211	0.521625045
41.5	27.5	31.9	35.6	29.3	31.6	108.6	63.1	32.9	26.4	24.2	5.0	0.302835052	0.521559924
70.6	66.0	169.3	44.6	59.5	48.0	88.3	146.4	76.3	37.1	109.5	46.6	0.864281401	0.52147379
147.0	202.2	172.6	149.1	143.0	287.7	231.6	353.6	183.6	47.2	57.0	55.6	0.792746114	0.519201403
349.3	352.2	313.5	650.6	433.1	217.9	1133.2	744.0	386.1	204.1	192.8	147.1	0.340710542	0.518937663
596.3	389.6	330.7	528.7	305.6	326.8	442.6	796.4	413.0	90.5	240.5	121.1	0.932967331	0.518533866
97.1	108.0	53.2	256.7	69.4	70.6	503.0	210.6	109.2	64.2	116.6	75.0	0.217048407	0.518311018
413.3	324.1	262.9	215.0	210.1	370.6	379.7	578.0	299.3	125.4	159.9	83.8	0.7883832	0.51789566
986.9	1161.5	957.4	559.5	1016.1	968.8	1186.9	1818.6	941.7	299.5	318.1	201.5	0.793424778	0.517821597
255.0	279.9	270.1	117.8	264.9	189.2	272.1	443.3	229.5	105.1	291.2	63.5	0.843440655	0.517693858
64.2	87.7	47.5	66.5	55.7	51.7	193.2	120.3	62.2	16.2	12.3	14.4	0.321965777	0.517093307
77.3	113.2	87.6	87.9	74.1	110.6	108.8	177.5	91.8	7.2	26.2	16.5	0.843596814	0.516972701
25.7	24.7	25.5	28.2	28.6	25.7	84.6	51.1	26.4	19.8	19.4	1.6	0.312204352	0.516634051
2962.5	2171.3	1979.0	1721.2	1510.0	2669.7	2704.0	4201.0	2169.0	793.6	756.8	557.0	0.802132412	0.516288824
43.3	65.9	40.4	49.7	56.0	28.6	151.5	91.7	47.3	57.8	52.2	13.0	0.312403715	0.516219361
593.9	799.0	807.3	469.7	596.0	1227.0	825.3	1455.2	748.8	233.7	336.8	268.3	0.907370606	0.514579897
170.6	152.6	103.8	130.7	88.9	215.1	170.1	279.1	143.6	26.0	105.1	46.2	0.84420801	0.514496907
1070.1	624.8	921.5	487.0	623.9	1210.4	948.3	1601.1	823.0	247.0	697.3	287.3	0.867852699	0.514003223
1020.6	555.5	712.6	414.8	586.8	918.6	898.2	1364.8	701.5	229.5	590.6	230.5	0.780987902	0.513974981
47.0	61.3	49.8	64.3	26.6	56.9	159.1	99.2	51.0	17.0	15.3	13.6	0.32036781	0.513944892
456.2	651.6	388.2	474.6	353.2	338.9	1326.6	863.6	443.8	299.7	157.0	115.4	0.334531904	0.513899826
1184.4	2089.8	1258.9	1903.8	643.7	624.8	5435.5	2499.5	1284.2	1354.8	895.5	614.6	0.236266007	0.51378787
530.9	603.0	418.1	497.5	467.6	350.3	1445.0	931.1	477.9	523.1	93.3	88.1	0.330726644	0.513241833
116.4	148.5	100.9	121.2	84.7	96.2	326.0	217.2	111.3	63.3	53.7	22.6	0.341420276	0.512413306
233.8	176.6	178.5	83.8	115.2	229.2	218.0	331.0	169.5	48.7	144.8	60.2	0.777456736	0.512165891
22.1	52.9	30.6	10.5	17.3	26.5	108.2	52.0	26.7	40.6	14.2	14.7	0.246257623	0.512106072
684.3	352.6	723.8	178.4	389.1	613.2	406.1	958.8	490.2	266.9	421.3	216.2	1.207173931	0.511288181
537.4	723.6	515.8	706.7	527.0	337.0	1808.5	1092.6	557.9	496.9	556.8	142.5	0.308503736	0.510613438
511.1	535.3	582.5	450.2	948.5	734.7	2285.5	1229.2	627.1	1067.6	626.2	184.4	0.274355295	0.510128539
69.4	67.7	61.1	79.4	30.4	63.9	188.6	121.6	62.0	33.0	20.8	16.7	0.328580011	0.509647536
38.3	115.8	81.6	121.8	67.3	45.6	309.0	154.2	78.4	101.8	83.9	34.9	0.253738106	0.508562532
1099.4	1346.6	848.4	945.6	1088.1	1085.6	3255.4	2103.2	1069.0	976.6	529.6	168.8	0.328358071	0.508259001
533.8	285.7	438.1	194.2	204.8	349.8	396.9	658.5	334.4	157.3	231.9	133.8	0.842614524	0.507805382
131.2	41.0	40.5	107.7	43.4	19.8	317.9	126.0	63.9	150.2	34.9	44.5	0.201136769	0.507407407
115.9	308.4	219.3	86.2	463.1	292.7	244.1	489.0	247.6	99.4	295.2	138.8	1.014255284	0.506298053
688.7	497.0	460.0	223.4	423.9	432.6	533.4	897.8	454.3	223.9	307.0	149.3	0.851643545	0.505955033
72.2	117.0	92.2	88.1	97.4	144.7	304.2	201.5	101.9	76.1	92.4	25.5	0.335130633	0.505772221
276.8	178.4	221.1	171.0	174.8	273.4	271.6	427.5	215.9	68.0	150.2	49.3	0.795038908	0.505068226
80.0	145.8	69.7	103.3	65.3	75.6	294.7	178.2	90.0	96.5	45.3	30.4	0.305246369	0.504769921
75.0	135.4	115.0	111.7	95.6	57.7	295.0	195.0	98.4	70.6	44.2	28.4	0.333559322	0.504511895
80.9	75.6	75.4	53.2	48.8	81.5	304.6	137.3	69.2	78.4	91.9	14.4	0.227307549	0.504322067
1470.2	1378.1	1087.5	1542.9	1064.6	779.8	4234.4	2420.6	1220.5	1296.0	803.9	292.3	0.288238397	0.504216551
540.2	603.4	802.9	526.4	412.7	1959.9	984.6	1602.1	807.6	307.7	548.8	579.0	0.820181318	0.504077981
1729.9	1318.7	1717.8	692.2	1373.9	1637.7	1751.1	2801.5	1411.7	414.6	786.8	393.4	0.806178973	0.503901426
31.4	37.1	30.0	33.6	16.9	18.7	213.2	55.5	28.0	121.2	22.3	8.2	0.131072969	0.503603604
2296.8	2885.6	2189.5	1293.5	1408.2	575.9	6045.7	3524.9	1774.9	3263.9	3895.8	834.5	0.293585261	0.503536743
20.6	14.8	9.8	34.4	13.5	10.6	105.2	34.3	17.3	27.4	14.4	9.2	0.164227797	0.50330033
857.4	511.2	712.6	436.8	320.6	814.0	725.6	1210.7	608.8	192.8	370.0	217.6	0.838937582	0.502822059
151.1	157.6	114.0	151.9	153.5	159.1	534.5	295.0	147.9	183.7	161.7	16.9	0.276655191	0.501310912
70.8	78.2	94.6	53.4	37.0	147.5	106.5	160.1	80.3	37.3	65.3	38.5	0.753804246	0.50118661
187.2	166.9	238.3	78.9	211.3	300.2	185.7	393.4	197.1	48.5	240.8	74.2	1.061340225	0.501101508
321.3	328.7	216.7	203.5	138.3	225.0	279.5	477.9	238.9	58.7	54.0	73.4	0.854677923	0.499972098
60.9	19.8	43.5	50.0	32.7	34.0	124.2	80.3	40.2	90.2	24.7	14.5	0.323320986	0.499751058
461.8	311.5	305.7	307.4	201.6	321.9	1082.9	637.2	318.3	506.1	202.7	83.1	0.29394292	0.499523989
226.2	240.4	195.4	244.0	245.9	224.4	718.1	459.4	229.4	194.9	190.0	19.0	0.3194487	0.499288959

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.29569.1.A1_at, CO942122, TRIO	36.5	68.5	37.4	69.5	41.3	31.1	36.7	34.4	30.7	26.4
Ssc.3299.1.S1_at, CK461574, TMEM106B	2626.9	3072.5	1765.0	4455.1	3787.1	2111.3	1882.1	2746.3	1255.6	2246.7
Ssc.29056.1.S1_at, CN070171, WDR43	372.2	679.4	475.9	95.6	419.6	947.3	721.4	273.8	1323.3	372.4
Ssc.7510.1.A1_at, BQ599023, ZNF33A	36.9	68.8	42.5	80.2	74.3	35.9	36.6	27.8	46.7	43.6
Ssc.20648.1.S1_at, CN165729, ASL	419.1	353.3	254.5	176.3	302.0	251.5	137.4	164.9	163.2	226.9
Ssc.20655.1.S1_at, BX676064, FAM78B	365.9	540.3	232.0	293.0	484.9	200.4	172.2	193.0	140.0	218.9
Ssc.5721.1.S1_at, CF176086, CDC45L	242.2	208.7	223.5	201.7	269.0	157.1	156.5	105.0	145.9	157.3
Ssc.6163.2.S1_at, BX922988, ETS2	249.2	469.1	579.9	294.5	344.1	1136.0	965.4	333.6	924.3	514.6
Ssc.21780.1.A1_at, BX665827, MYO1E	967.6	798.9	1242.3	591.8	970.7	1574.5	1153.6	876.2	1946.2	1350.9
Ssc.24440.1.A1_at, CK462370, CAB39L	285.9	239.8	209.5	347.6	308.4	144.6	198.1	197.7	165.8	148.9
Ssc.4641.1.A1_at, CK455585, PXK	523.7	640.8	443.1	574.2	530.2	744.8	1127.3	705.5	1345.2	864.0
Ssc.3393.2.A1_a_at, CK467687, PHCA	964.9	971.5	916.3	339.6	760.6	1501.9	1574.0	980.6	1343.2	1163.2
Ssc.12682.1.A1_at, CK463811, VAV3	104.8	103.4	126.4	232.2	357.3	82.2	93.3	150.9	53.1	93.0
Ssc.3791.1.S1_at, BI182343, CTSF	3214.1	3394.7	2979.7	3888.0	3228.3	1840.6	2224.5	3084.9	1504.7	2174.5
Ssc.2545.2.A1_at, BQ604556, TMEM165	1769.7	2023.6	2229.7	1201.4	1818.7	2099.8	3399.9	2195.6	3677.6	2233.2
Ssc.2337.1.S1_at, CN158060, PTPRF	292.7	433.6	724.6	537.6	333.5	739.4	906.1	722.6	485.4	935.7
Ssc.19276.1.S1_at, CK461869, KCNH1	193.1	166.9	154.5	59.7	106.4	232.6	447.4	169.5	553.3	161.8
Ssc.21721.1.A1_at, CF794794, NIF3L1	103.1	99.4	64.3	72.2	148.1	275.8	105.8	114.1	114.8	168.5
Ssc.22266.1.A1_at, CF789721, PCDHB16	42.3	63.3	112.0	136.1	80.4	48.6	29.2	71.7	28.4	15.9
Ssc.17931.1.S1_at, CF177606, ZNF76	122.2	91.1	66.4	98.5	115.2	55.1	45.3	78.5	66.1	65.0
Ssc.25948.1.S1_at, BX925423, RNF157	343.3	458.2	457.0	290.8	268.4	809.6	1578.7	799.3	1469.0	737.9
Ssc.8496.1.A1_at, BF703133, PLXDC2	150.9	138.7	195.6	279.4	228.2	117.1	163.4	173.4	83.4	87.6
Ssc.11998.1.A1_at, BI184543, PRKAG3	241.8	162.0	196.8	216.2	193.5	342.7	328.3	353.6	366.0	305.9
Ssc.15325.1.S1_at, CN160539, MAF	347.2	477.4	288.3	1380.5	1088.0	334.6	210.0	440.9	77.1	225.6
Ssc.9834.2.S1_at, CB471302	39.5	35.6	31.7	80.9	54.9	35.1	21.6	35.6	31.4	33.5
Ssc.30068.1.A1_at, CO949669, ADAM18	261.5	272.8	157.7	266.0	476.2	138.0	92.2	169.4	112.1	279.4
Ssc.18496.1.S1_at, CF175485, METAP1	402.5	347.7	415.0	222.5	337.4	467.7	609.7	310.5	817.2	392.2
Ssc.19040.2.S1_at, CF366839, ARHGAP12	225.2	297.7	368.4	92.8	193.2	281.0	113.2	91.3	101.9	181.1
Ssc.9404.2.S1_at, CK468342, SARS	3095.4	2838.7	3372.4	1960.0	2264.5	3844.7	4593.1	4258.2	5820.5	2891.9
Ssc.5639.2.S1_at, BP143734, MACF1	505.9	439.4	315.0	187.4	359.8	968.0	533.0	398.9	711.7	566.4
Ssc.3550.1.S1_at, BQ600694, TM4SF1	5664.3	4552.7	6170.2	2762.1	3112.5	7172.3	9570.1	8361.4	9593.6	4957.5
Ssc.13470.1.A1_at, BQ602386	35.6	112.5	47.7	90.4	60.1	39.6	39.0	55.5	45.2	49.4
Ssc.5257.1.S1_at, CK449202, B3GNT1	770.8	966.8	1006.3	1143.9	958.5	1172.2	1811.3	1306.0	2113.1	1127.2
Ssc.15683.1.A1_at, CN156995, PCDHGC5	1797.8	1537.8	1947.9	3118.0	2711.9	1236.6	1367.4	1720.8	898.2	1497.3
Ssc.24513.1.S1_at, CK463492	2314.4	1870.0	1639.9	3215.4	2668.2	1253.5	1245.5	2005.3	1157.6	1470.4
Ssc.7943.1.S1_at, BQ599827, APEX1	2096.1	1881.5	2469.4	1178.9	1207.1	2364.1	3395.9	2688.2	3214.0	2177.9
Ssc.22447.1.S1_at, CK466188, MKL2	1907.9	2343.3	1131.9	2269.5	3180.4	617.4	1831.3	1374.8	873.0	1108.2
Ssc.1897.1.A1_at, CN160243, ALG13	955.9	1450.4	733.3	1931.6	1671.0	694.2	932.0	785.9	481.2	856.7
Ssc.30637.1.A1_at, CO940830, SLC39A11	701.0	719.5	452.8	884.8	964.1	230.1	192.2	408.2	211.9	570.7
Ssc.2572.1.S1_at, BQ604031, PPA1	4093.5	4011.3	4648.8	1960.8	2450.9	5780.0	7198.3	4163.2	7734.0	4849.8
Ssc.29481.1.A1_at, CO956104	89.3	77.7	121.7	100.8	38.0	129.5	184.0	182.5	99.8	78.9
Ssc.25907.1.S1_at, BX924773, VAV3	37.1	37.9	41.6	89.8	89.9	36.5	29.4	49.9	36.8	32.5
Ssc.7269.1.A1_at, BQ598412, ST6GALNAC2	703.1	441.8	554.0	578.7	652.9	335.2	318.6	244.0	161.1	493.2
Ssc.10992.1.S1_a_at, CN160594, WBSCR22	1616.6	1564.7	1771.8	952.1	1196.6	1853.5	2378.1	1744.8	3191.3	1601.2
Ssc.3948.2.A1_at, CK460322, DMD	115.1	132.5	56.2	183.8	194.0	60.8	72.7	66.1	31.6	69.0
Ssc.4843.1.A1_at, AW414489, BBS2	264.6	434.1	124.7	276.4	383.8	296.3	92.2	132.6	72.8	268.0
Ssc.507.1.A1_at, AF152021.1, TYROBP	558.1	366.0	396.5	1000.2	899.4	204.8	125.2	587.3	201.9	298.9
Ssc.26268.1.S1_at, BX923286	493.2	605.7	909.9	549.7	447.8	555.1	1037.0	478.0	2290.6	804.5
Ssc.30705.1.A1_at, CO950276, PPFIA2	299.3	279.6	146.2	237.2	299.0	115.1	150.0	129.9	123.6	197.9
Ssc.28443.1.A1_at, CN032159, ZNF618	83.1	94.3	91.9	150.5	174.9	61.0	38.8	88.0	34.0	70.2
Ssc.22443.1.S1_at, BG383630, TSR1	686.8	944.5	885.0	645.2	1229.1	471.1	599.2	618.5	454.2	475.7
Ssc.26386.1.A1_at, BF703676, NIP7	306.6	429.6	422.5	242.1	204.9	429.2	758.4	400.2	1114.8	335.7
Ssc.9212.1.A1_at, BF709894	2834.6	1762.5	3354.7	1814.6	1488.7	4519.8	4059.3	3250.0	6630.4	2615.8
Ssc.8865.1.A1_at, CK458594, DUSP6	1326.9	1813.6	2045.2	2476.4	2684.2	1094.2	1656.1	1569.7	904.4	1254.8
Ssc.140.1.S1_at, NM_214037.1, AMBN	354.8	334.3	257.7	449.2	855.4	242.9	132.3	216.0	188.1	131.5
Ssc.11609.1.A1_at, BI182003, ASNS	2666.0	2556.3	2283.3	1776.9	2016.8	2553.3	4802.5	3192.5	6726.2	2160.3
Ssc.4538.1.S1_at, CK465820, PRSS23	1793.1	1032.9	1598.3	396.3	1897.5	1779.9	1781.0	2519.5	4229.1	4407.5
Ssc.29259.1.A1_at, CO953119, ZNF567	253.7	376.9	189.0	558.8	361.9	209.6	163.3	193.5	98.1	232.9
Ssc.15398.1.A1_at, CF788937, ARHGAP30	190.2	187.6	199.9	392.1	301.6	136.3	75.9	123.9	82.8	125.6
Ssc.16630.1.S1_at, NM_213739.1, PAQR7	294.9	255.4	225.6	154.7	186.1	303.1	487.0	470.7	288.8	337.6
Ssc.30372.1.A1_at, CO990888, BRWD1	89.4	129.2	119.7	148.0	100.4	62.2	122.7	86.7	52.3	61.3

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
12.2	29.2	6.6	16.7	20.1	10.6	50.6	31.9	15.9	16.9	3.9	8.0	0.313981043	0.49905838
810.4	1195.7	783.8	1386.7	1220.2	733.0	3141.3	2048.4	1021.6	1037.6	544.6	278.4	0.325224216	0.49874699
393.9	463.5	401.4	187.2	225.8	504.9	408.5	727.6	362.8	210.5	428.7	128.4	0.887999543	0.498575303
17.1	22.9	15.4	16.9	22.1	19.6	60.5	38.1	19.0	19.5	7.4	3.0	0.313842088	0.498426023
109.6	120.8	88.1	91.3	72.7	81.7	301.0	188.8	94.0	92.7	48.1	17.9	0.312361591	0.498110676
66.0	174.3	85.5	80.4	62.3	83.8	383.2	184.9	92.1	128.8	30.2	41.4	0.240201451	0.497836668
89.4	79.0	101.5	89.6	38.5	32.2	229.0	144.4	71.7	27.2	22.5	29.1	0.313073094	0.496674979
351.6	408.0	379.3	239.4	241.7	688.5	387.4	774.8	384.8	135.4	336.0	164.6	0.993262082	0.496592581
886.2	517.7	778.8	292.1	586.0	1048.0	914.3	1380.3	684.8	240.3	407.5	273.2	0.749021066	0.49613122
108.2	55.0	99.5	81.5	84.0	80.8	278.2	171.0	84.8	54.7	25.8	18.3	0.304892659	0.496043348
640.2	358.8	499.6	343.9	463.8	540.5	542.4	957.4	474.5	72.5	272.3	112.2	0.874754179	0.495599008
751.1	598.7	597.1	692.2	484.1	778.9	790.6	1312.6	650.4	266.1	243.7	111.0	0.822623896	0.495474562
65.7	32.5	24.0	96.6	31.1	30.6	184.8	94.5	46.8	110.0	35.5	28.5	0.252948815	0.494708995
1295.4	1239.8	968.6	1221.4	869.0	827.6	3341.0	2165.8	1070.3	339.6	589.7	205.9	0.320357023	0.494173161
1913.9	949.7	1458.0	863.4	1109.8	1771.5	1808.6	2721.2	1344.4	385.3	754.3	438.6	0.743319953	0.494036988
462.2	249.2	243.6	360.7	499.1	431.5	464.4	757.8	374.4	173.7	179.9	109.1	0.806165662	0.494013688
192.5	165.4	150.4	99.2	137.0	182.2	136.1	312.9	154.5	53.0	177.3	33.8	1.134660594	0.493576633
51.3	116.8	46.4	92.0	39.7	114.4	97.4	155.8	76.8	32.9	71.6	35.2	0.787996989	0.492725717
15.9	18.8	15.1	15.2	36.4	13.1	86.8	38.8	19.1	37.5	21.8	8.7	0.219803425	0.492346061
44.7	29.1	25.2	43.0	17.0	24.0	98.7	62.0	30.5	21.9	12.5	11.1	0.309079854	0.491935484
573.3	397.0	721.4	290.5	746.1	451.1	363.5	1078.9	529.9	90.1	408.9	182.5	1.457611267	0.491148392
48.6	76.7	60.1	65.1	79.2	38.0	198.6	125.0	61.3	57.6	41.9	16.0	0.308638867	0.490345122
147.9	109.2	173.5	134.4	309.3	123.4	202.1	339.3	166.3	29.5	23.3	73.4	0.822940381	0.490077611
328.7	19.5	85.1	187.5	109.8	26.8	716.3	257.6	126.2	488.8	137.3	116.6	0.17623462	0.489960151
16.6	16.1	11.4	31.1	10.7	6.3	48.5	31.4	15.4	20.1	5.7	8.6	0.316707887	0.488761662
50.0	89.3	54.9	147.1	78.0	44.3	286.8	158.2	77.3	116.0	73.7	38.3	0.269372008	0.488349555
336.2	242.0	294.7	153.5	187.8	306.3	345.0	519.5	253.4	76.3	199.6	71.8	0.734498483	0.487846353
94.2	63.4	58.9	90.8	75.2	66.8	235.5	153.7	74.9	104.6	79.3	14.7	0.318029956	0.487204511
2511.9	2030.6	2288.9	1516.4	1763.7	2396.8	2706.2	4281.7	2084.7	584.1	1071.0	387.4	0.770348336	0.486892217
450.4	291.4	324.9	234.5	248.7	302.7	361.5	635.6	308.8	121.9	216.6	77.2	0.854126325	0.485787707
4624.6	2283.8	3068.8	1763.5	2759.9	8590.4	4452.4	7931.0	3848.5	1506.8	1939.9	2517.0	0.864373052	0.485248986
27.3	22.3	26.8	13.2	19.3	23.8	69.3	45.7	22.1	31.6	6.9	5.3	0.319328136	0.483530098
754.8	664.0	912.7	407.5	698.1	929.5	969.3	1506.0	727.8	133.6	434.9	191.4	0.750847726	0.483257634
674.4	631.4	728.1	536.0	719.5	605.7	2222.7	1344.1	649.2	664.5	306.7	73.2	0.292072333	0.483001751
792.2	640.5	587.8	811.9	690.0	610.2	2341.6	1426.5	688.8	629.6	343.5	94.4	0.294146118	0.482850319
1853.9	919.5	1430.7	898.6	1074.2	1838.8	1766.6	2768.0	1336.0	564.4	527.0	438.9	0.75622665	0.482637409
656.1	840.7	435.3	670.3	357.4	393.3	2166.6	1160.9	558.9	742.8	468.0	192.1	0.257938706	0.48137716
311.6	552.3	292.9	446.8	247.0	309.7	1348.4	750.0	360.1	496.7	174.0	115.5	0.267012251	0.480066667
154.0	225.8	119.9	240.3	64.8	124.3	744.4	322.6	154.9	197.2	163.3	67.2	0.208008705	0.479976443
3325.7	1888.7	2492.4	1770.2	2208.5	5427.8	3433.1	5945.1	2852.2	1159.8	1514.3	1378.5	0.830808861	0.479762469
101.0	65.5	68.5	32.3	43.5	76.8	85.5	134.9	64.6	31.1	47.6	24.4	0.755555556	0.478731288
34.3	16.4	16.9	18.3	10.1	10.3	59.3	37.0	17.7	28.0	7.8	8.8	0.298965013	0.478570142
231.3	187.1	156.8	134.0	79.6	101.6	586.1	310.4	148.4	100.1	123.3	55.8	0.253199113	0.478061981
1335.5	906.8	1097.6	730.4	792.3	1307.3	1420.4	2153.8	1028.3	336.2	649.9	259.3	0.723983122	0.477447403
32.0	34.0	25.3	34.0	26.8	19.8	136.3	60.0	28.7	55.8	16.5	5.7	0.210167254	0.477181879
72.5	209.0	11.8	69.8	53.6	76.3	296.7	172.4	82.2	119.9	103.0	66.5	0.276916509	0.476660092
238.5	62.1	89.4	224.0	103.6	93.0	644.0	283.6	135.1	290.7	180.6	75.9	0.20976958	0.476341584
617.9	588.9	670.4	206.9	223.2	640.9	601.3	1033.0	491.4	182.5	736.6	215.8	0.817228265	0.475651153
64.9	109.5	50.0	48.6	67.6	68.2	252.3	143.3	68.1	64.5	33.1	22.1	0.270091704	0.475459409
37.9	22.1	30.5	30.2	27.0	18.5	118.9	58.4	27.7	41.1	22.4	6.9	0.232890533	0.474315068
303.8	274.4	274.6	206.7	277.5	153.5	878.1	523.7	248.4	233.7	78.4	56.6	0.282896035	0.474312954
454.3	282.3	362.8	120.9	153.4	353.6	321.1	607.7	287.9	102.5	327.4	129.3	0.896441843	0.473757255
2717.8	1486.0	2224.8	804.5	1694.1	3026.7	2251.0	4215.1	1992.3	801.4	1536.2	825.4	0.885072841	0.472666265
634.3	763.4	534.0	540.6	726.5	473.6	2069.3	1295.8	612.1	538.7	316.4	115.6	0.295790121	0.472331975
115.2	34.6	52.3	155.5	90.5	68.1	450.3	182.2	86.0	236.5	49.8	44.3	0.191066299	0.472295418
2584.0	1241.2	2426.3	999.0	1399.7	2360.3	2259.9	3887.0	1835.1	369.4	1880.3	696.8	0.812034079	0.472112739
1460.9	454.4	1784.6	1216.1	1649.6	1753.0	1343.6	2943.4	1386.4	626.0	1292.4	503.1	1.031864168	0.471031234
82.9	100.7	78.8	69.7	69.7	104.7	348.1	179.5	84.4	141.1	52.1	15.1	0.242534812	0.470340242
78.7	28.5	50.0	75.4	31.5	42.7	254.3	108.9	51.1	90.5	27.5	21.5	0.201090661	0.469543924
195.2	252.7	273.7	79.3	110.2	152.0	223.3	377.4	177.2	55.3	94.4	77.5	0.793334527	0.469434435
46.4	32.4	37.1	37.9	15.5	47.6	117.3	77.0	36.2	23.2	28.5	11.7	0.308079086	0.46923676

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.3596.1.S1_at, CK455114, PTRH2	1080.6	1006.3	1025.6	920.9	963.5	1115.2	1687.8	1559.4	2444.8	1381.5
Ssc.3645.1.S1_at, BG382103, PLVAP	2319.1	715.5	897.3	1293.1	1351.0	772.5	729.5	764.6	796.9	909.0
Ssc.22443.2.A1_at, AJ658976, TSR1	244.5	242.1	222.6	123.8	146.5	290.9	375.4	235.8	697.0	245.1
Ssc.15594.1.S1_at, BG610612, COTL1	71.2	37.7	41.2	39.7	36.6	54.7	60.2	50.3	60.4	131.4
Ssc.20188.2.S1_at, BX676751	756.6	405.1	375.7	681.1	546.2	389.6	262.4	354.7	462.9	239.3
Ssc.1567.3.A1_at, CN159325, PDCD11	1059.7	895.8	1032.6	420.1	524.2	1150.6	2125.5	1062.0	2253.4	1085.2
Ssc.27560.1.S1_at, CN162190, SERPINC1	179.0	235.6	190.8	245.0	325.2	181.3	141.4	119.9	91.7	142.6
Ssc.6139.1.S1_at, CF360612, WARS	1239.7	1704.1	774.6	759.5	1091.8	1585.2	1328.6	1635.4	2470.0	1534.5
Ssc.18468.1.S1_at, CN156222, SNX17	867.9	614.6	686.7	899.9	893.9	488.9	393.2	573.8	437.4	731.7
Ssc.11995.1.A1_at, CB476520, MTHFD2	522.6	549.7	583.6	467.0	368.1	858.5	1200.6	702.5	1103.4	565.4
Ssc.24865.2.A1_at, CF787459, XPO5	235.0	289.5	180.4	222.1	261.9	292.3	531.0	183.5	491.1	340.0
Ssc.25253.1.S1_at, BX926557, FRRS1	224.5	646.8	428.8	184.1	162.9	319.8	284.3	134.3	150.9	75.8
Ssc.8139.1.S1_at, CB475937, PHYH	954.7	1255.5	558.2	937.5	1413.2	707.3	402.5	811.9	312.3	1142.5
Ssc.24035.1.S1_at, BG895856, EIF2C2	1344.9	1006.6	1724.7	633.0	794.4	1919.9	2747.2	1385.7	3020.3	1434.4
Ssc.6798.1.S1_at, BQ604492, HSPA9	1860.6	1664.4	1924.5	1107.3	1035.2	2028.6	2616.9	2013.8	2914.7	1954.8
Ssc.25004.1.S1_at, CK464684, IGF1	428.0	725.0	208.5	462.9	466.2	158.5	51.3	191.5	36.1	249.9
Ssc.19537.1.S1_at, CN070423, IRF2	890.2	822.2	807.4	1883.0	1245.8	668.8	537.8	1017.1	331.9	889.3
Ssc.10388.1.S1_a_at, CN164439, PPAN	225.1	308.9	195.5	70.4	184.4	379.7	444.7	191.8	639.0	232.8
Ssc.5910.1.A1_at, CF368319, VAV1	188.5	189.8	197.7	241.8	423.0	134.1	71.8	155.8	106.0	140.1
Ssc.9288.1.A1_at, BF710115, STAMBPL1	49.8	52.7	36.4	85.8	81.9	31.0	10.8	52.3	42.1	51.7
Ssc.902.1.S1_a_at, CK463733, CCT3	1733.1	1624.5	2017.0	602.0	1251.8	2253.0	2535.1	1336.6	3161.1	1671.9
Ssc.19975.1.S1_at, BX675500, PTGES3	1756.8	1950.7	2368.8	1465.0	1441.2	2818.0	3195.3	1856.0	3471.2	2297.6
Ssc.19032.1.A1_at, CB478236, ZC3H7A	450.7	609.9	352.8	289.2	444.6	554.4	974.4	497.7	787.2	678.5
Ssc.11715.1.A1_at, CF363273, NENF	1145.6	1165.3	915.2	1114.0	1453.2	771.6	590.4	946.1	560.2	935.2
Ssc.5530.2.S1_at, BG385253, ZNF205	126.0	136.5	119.1	175.3	311.4	80.4	72.8	128.5	38.1	114.5
Ssc.19483.3.A1_at, CF365027, MPV17	205.3	184.9	146.7	181.6	236.9	115.6	83.0	159.9	51.8	140.6
Ssc.2571.1.S1_at, BF080937, PLD3	2456.9	2431.0	2152.0	2407.3	3300.7	1663.4	1400.0	1811.4	1652.6	1954.5
Ssc.17462.1.S1_at, CN070334, AQP11	85.0	80.8	59.6	94.0	143.1	50.0	45.9	78.3	43.4	63.0
Ssc.15615.1.S1_a_at, BX676781, TARS	878.8	944.2	909.8	588.0	681.4	1507.1	1842.3	1059.4	2057.1	1007.8
Ssc.4915.1.A1_at, BF710057, NTRK3	189.1	284.6	292.3	368.4	136.0	92.6	264.7	194.4	106.6	103.1
Ssc.30812.2.S1_at, AJ655463, SPAG7	518.6	425.2	290.2	152.5	579.5	293.1	310.5	204.7	216.7	283.0
Ssc.7968.1.S1_at, BM484493, MEST	863.1	1101.0	836.9	1520.4	1309.2	742.8	600.6	925.9	329.5	623.4
Ssc.22221.1.S1_a_at, CK457408	600.2	412.9	524.1	306.4	254.1	524.9	590.9	441.5	901.3	739.1
Ssc.11457.1.A1_at, BQ602829, PPT1	2353.8	3157.3	2540.6	3862.5	3865.9	2206.6	1584.8	2621.6	1753.0	2202.9
Ssc.7516.1.A1_at, BQ599047, FGFR2	180.3	119.7	42.8	237.4	314.4	124.6	79.4	103.5	55.9	177.9
Ssc.20835.1.S1_at, BX676283, TMEM201	154.7	90.1	140.8	119.5	83.9	152.6	219.1	143.2	247.6	137.6
Ssc.14532.1.S1_at, D86723.1, FUT8	338.5	398.0	254.1	202.5	619.5	258.3	243.3	198.7	141.7	254.2
Ssc.2487.1.S1_at, BQ604572, AIFM2	401.9	459.8	261.6	513.3	587.7	256.6	254.3	346.4	225.2	294.5
Ssc.13603.1.S1_at, CK456592, C14orf101	443.9	513.6	323.4	529.0	554.7	328.4	239.4	334.6	160.0	415.0
Ssc.3426.1.A1_at, CO946769, MAPK6	1406.1	1593.7	1597.7	1531.6	1258.3	2263.2	2679.7	1844.2	2845.4	1851.4
Ssc.22256.2.A1_at, CF789027, ENTPD4	115.4	97.2	178.5	73.8	76.0	229.7	209.0	212.1	284.0	153.0
Ssc.6681.1.A1_at, BM190253, DDX39	1158.8	1046.9	1525.9	672.6	811.2	1341.4	1989.3	1332.0	2876.5	1085.4
Ssc.13849.1.S1_at, BI399153, TINAGL1	652.3	450.9	1116.2	397.5	339.8	1038.0	648.0	684.1	828.3	1261.5
Ssc.23964.1.S1_at, CK467047, KRIT1	251.4	197.8	198.6	262.7	242.7	178.9	161.9	123.7	131.2	169.9
Ssc.10998.1.A1_at, CK465529, CLK1	2209.8	2895.3	2040.0	2282.0	2019.4	1294.0	1367.3	1566.1	1660.0	1293.4
Ssc.1321.1.S1_at, BQ602783, RNASE11	1019.4	1212.6	934.0	1076.8	1165.7	633.0	759.4	773.2	417.6	928.3
Ssc.16634.1.S1_at, NM_213958.1, TLR9	124.1	76.6	77.5	180.8	198.4	43.9	49.8	76.4	27.8	54.8
Ssc.283.1.S1_at, NM_214076.1, KMO	234.8	258.3	206.1	209.7	528.1	73.6	95.5	253.5	99.0	125.3
Ssc.4033.2.S1_at, CK467457, ARSE	415.9	443.2	681.2	541.6	482.0	318.4	281.3	351.2	291.2	408.7
Ssc.29178.1.A1_at, BI233963, TGOLN2	1131.0	1028.5	710.8	1615.3	1315.0	709.3	598.9	1124.0	473.1	954.3
Ssc.8429.1.S1_at, CK457455, BCAP29	1387.4	1757.9	1193.5	2152.7	1863.2	1090.4	931.0	1090.0	799.8	1476.1
Ssc.25441.2.S1_a_at, AJ653657, C12orf35	1976.1	2121.8	1879.8	3053.7	2353.8	1187.2	1161.6	1401.5	1244.8	1855.6
Ssc.9718.1.A1_at, CN160375, CITED2	1897.9	1753.4	1059.8	1891.3	1782.3	751.8	576.5	980.3	406.4	469.8
Ssc.26412.1.S1_at, CK457910, PLAG1	262.9	199.8	186.7	183.5	261.3	339.5	390.6	163.8	738.9	325.1
Ssc.5410.1.S1_at, CN159595, TADA3L	262.3	186.1	223.4	223.8	300.1	193.5	74.5	197.9	97.0	131.8
Ssc.575.1.S1_at, NM_214209.1, ACP5	178.9	102.7	136.0	112.7	239.0	61.1	89.5	159.4	44.9	84.7
Ssc.2296.1.A1_at, BQ602371, C14orf101	149.4	123.9	68.1	140.4	136.6	65.1	64.2	73.7	56.9	128.0
Ssc.21291.1.A1_at, CF795040, GABPB2	353.0	291.2	189.8	445.0	326.7	169.8	233.2	170.1	212.8	238.6
Ssc.1647.1.S1_at, BI401726, C11orf60	461.3	452.6	374.2	618.7	579.5	286.3	179.7	297.5	110.8	307.0
Ssc.25207.1.A1_at, CK460874, ITGA6	845.8	347.9	613.0	247.2	350.4	306.2	351.0	168.7	318.7	317.9
Ssc.21663.1.A1_at, BX915625, LIPG	76.5	116.4	183.2	197.0	171.4	156.0	280.1	500.4	143.6	143.6

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
1049.0	649.0	808.6	550.7	540.4	1011.4	999.4	1637.7	768.2	60.8	499.7	225.0	0.768659902	0.469050846
326.2	727.6	490.6	202.9	165.5	320.6	1315.2	794.5	372.2	621.3	68.4	208.1	0.283024128	0.468512691
280.9	120.2	188.4	76.1	90.9	280.3	195.9	368.8	172.8	56.7	191.6	92.0	0.882082695	0.468495825
46.6	16.3	46.5	20.9	24.4	46.0	45.3	71.4	33.5	14.6	33.8	14.4	0.738736749	0.468487395
128.2	228.4	95.4	199.0	171.0	138.7	552.9	341.8	160.1	166.7	92.1	48.9	0.289573311	0.468478749
1140.9	536.6	728.2	549.6	499.6	855.3	786.5	1535.3	718.4	295.9	599.7	247.7	0.913394704	0.467887677
61.4	85.9	56.0	67.3	65.9	43.0	235.1	135.4	63.3	57.7	33.0	14.2	0.269011569	0.467203427
703.8	613.3	643.0	796.0	501.2	1531.1	1113.9	1710.7	798.1	389.0	440.2	372.2	0.716435954	0.466503774
249.0	319.1	216.7	263.3	165.1	254.5	792.6	525.0	244.6	132.6	133.7	51.2	0.30862562	0.465936508
492.3	389.6	451.6	301.2	319.3	522.1	498.2	886.1	412.7	84.3	266.2	91.1	0.828348722	0.46574049
151.4	194.1	182.7	144.7	174.6	179.1	237.8	367.6	171.1	41.2	143.4	19.1	0.719572714	0.465476903
96.1	96.2	61.6	119.5	89.9	75.4	329.4	193.0	89.8	206.4	104.1	19.8	0.272549734	0.465150416
187.4	413.7	271.9	590.9	214.6	205.0	1023.8	675.3	313.9	329.5	333.2	158.9	0.306613142	0.464855126
1432.7	734.1	1118.7	414.3	792.6	1365.3	1100.7	2101.5	976.3	438.9	750.2	397.0	0.886949754	0.464564993
1600.0	1095.8	1092.1	730.1	793.6	1112.4	1518.4	2305.8	1070.7	420.1	433.8	308.5	0.705128205	0.464344367
108.3	57.1	41.4	103.1	37.9	34.8	458.1	137.5	63.8	183.4	91.8	33.4	0.13919206	0.463892526
313.3	404.5	238.6	306.5	298.5	346.5	1129.7	689.0	318.0	457.4	273.2	55.0	0.281470925	0.461527669
184.6	148.2	135.6	140.2	121.3	310.8	196.9	377.6	173.5	85.9	179.1	70.5	0.881083003	0.459348517
99.0	35.6	42.3	77.4	49.6	31.1	248.2	121.6	55.8	100.2	33.1	26.7	0.224989254	0.45930679
24.2	11.2	12.8	22.7	23.5	9.0	61.3	37.6	17.2	21.5	17.3	7.0	0.281039356	0.458577257
1419.0	650.8	981.0	767.5	566.8	1643.2	1445.7	2191.5	1004.7	545.5	718.1	436.6	0.694978603	0.458452352
1843.3	1034.1	1319.6	758.2	743.6	1796.6	1796.5	2727.6	1249.2	383.7	656.6	490.0	0.695370628	0.457993904
369.3	510.4	304.2	213.8	251.9	265.4	429.4	698.4	319.2	121.2	190.7	107.5	0.743215971	0.456970773
343.9	400.2	271.0	438.8	432.2	194.9	1158.7	760.7	346.8	192.5	183.1	97.4	0.299340042	0.455939705
59.6	23.7	31.5	61.7	33.5	27.3	173.7	86.9	39.6	80.0	35.8	16.7	0.227743867	0.455330417
37.3	64.8	44.4	68.7	38.8	45.8	191.1	110.2	50.0	33.2	43.5	13.4	0.261496057	0.453500333
998.1	805.2	785.0	891.8	503.1	612.3	2549.6	1696.4	765.9	437.4	206.6	181.3	0.300408956	0.451500646
32.9	33.7	24.3	19.0	13.9	28.0	92.5	56.1	25.3	31.0	14.5	7.8	0.273513514	0.450819672
809.9	636.7	700.0	399.2	498.5	997.0	800.4	1494.7	673.6	156.6	464.7	215.0	0.841474689	0.450613485
39.8	47.3	61.8	62.4	173.7	26.5	254.1	152.3	68.6	91.7	75.0	53.3	0.269928107	0.450376499
118.2	120.6	89.3	170.7	91.6	116.4	393.2	261.6	117.8	173.2	47.7	29.3	0.299593082	0.45030581
172.1	361.7	151.2	440.8	329.0	286.2	1126.1	644.4	290.2	292.6	218.2	111.9	0.257669402	0.450261726
427.7	262.0	311.3	188.9	203.2	334.1	419.5	639.5	287.9	144.7	182.5	89.3	0.686148321	0.450115187
1026.8	1089.3	757.7	1154.4	864.7	702.5	3156.0	2073.8	932.6	711.6	411.2	184.8	0.295488199	0.449694117
42.4	50.2	68.4	48.3	60.2	22.3	178.9	108.3	48.6	104.7	46.7	15.9	0.271816082	0.449227169
93.0	77.5	86.0	46.7	70.0	112.0	117.8	180.0	80.9	30.9	50.0	22.1	0.68647425	0.449209347
109.2	165.2	70.8	130.1	27.5	87.0	362.5	219.2	98.3	162.2	49.4	48.0	0.271157453	0.448367086
109.2	109.4	101.5	190.8	110.7	117.7	444.9	275.4	123.2	123.2	46.7	33.5	0.276978525	0.447409828
107.3	179.8	103.5	149.3	61.3	189.8	472.9	295.5	131.8	93.1	98.0	49.7	0.278764555	0.446166689
1302.9	945.6	1079.5	673.6	781.7	1364.5	1477.5	2296.8	1024.6	144.9	461.5	277.3	0.693500645	0.446117318
104.7	80.9	166.3	43.0	54.2	132.8	108.2	217.6	97.0	42.8	47.0	47.2	0.896499661	0.44577741
993.1	669.0	815.0	494.0	536.9	1102.7	1043.1	1724.9	768.5	330.7	725.7	246.2	0.736712429	0.445498922
422.6	283.8	393.0	389.9	587.1	306.5	591.3	892.0	397.2	316.1	257.2	107.6	0.671610241	0.445245409
62.1	67.4	71.1	59.0	52.0	95.8	230.6	153.1	67.9	30.5	24.3	15.2	0.294398196	0.443443051
597.7	762.3	593.3	698.8	716.4	439.3	2289.3	1436.2	634.6	356.6	167.6	116.9	0.277217199	0.441895982
321.4	378.0	265.9	438.0	234.1	224.4	1081.7	702.3	310.3	111.7	190.5	85.1	0.286863271	0.441833974
37.6	10.6	29.8	12.0	29.8	13.9	131.5	50.5	22.3	56.8	17.7	11.5	0.169480783	0.440904894
94.2	10.8	30.1	117.4	39.2	50.2	287.4	129.4	57.0	136.2	71.8	40.6	0.198271863	0.440433864
186.1	165.5	157.6	144.5	98.3	118.1	512.8	330.2	145.0	105.3	51.6	32.2	0.282804842	0.439231484
326.1	452.5	275.8	369.3	362.0	242.5	1160.1	771.9	338.0	335.9	264.8	74.6	0.291377903	0.437912392
458.2	529.1	416.4	629.2	367.8	428.7	1670.9	1077.5	471.6	382.4	253.9	93.8	0.282216397	0.437665126
602.8	636.2	616.7	806.8	493.5	437.7	2277.0	1370.1	599.0	469.5	286.9	128.1	0.263038857	0.437145109
310.3	189.8	240.2	449.5	347.3	133.5	1676.9	637.0	278.4	350.9	232.3	114.3	0.166036551	0.437128443
128.5	195.7	192.7	122.2	169.4	217.9	218.8	391.6	171.1	40.0	211.9	38.7	0.781697435	0.436862625
68.2	50.8	51.1	62.0	70.3	61.5	239.1	138.9	60.7	43.4	55.7	8.3	0.253617128	0.436519361
46.4	11.6	32.0	92.7	34.2	13.3	153.9	87.9	38.4	55.9	43.9	29.7	0.249360891	0.436381559
37.4	53.0	29.3	37.9	23.9	21.6	123.7	77.6	33.9	32.4	28.8	11.5	0.273690168	0.436323795
84.2	137.7	90.0	87.0	69.0	67.4	321.1	204.9	89.2	92.9	33.3	25.6	0.277812377	0.43541565
93.3	139.2	78.6	139.1	86.7	79.6	497.3	236.3	102.8	99.9	86.9	28.7	0.206632345	0.434902226
98.7	160.2	118.6	106.4	101.4	177.6	480.9	292.5	127.2	244.9	71.2	33.5	0.264422077	0.434700855
91.7	57.6	122.0	53.4	130.6	182.7	148.9	244.7	106.3	50.7	154.1	49.1	0.714125812	0.434474681

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.22994.1.S1_at, BX672348, ST3GAL6	200.6	189.8	195.4	225.7	255.0	47.0	119.9	239.0	67.3	125.2
Ssc.27366.1.S1_at, BF194676, GTF2IRD2	273.6	203.8	114.5	88.9	236.4	117.6	73.1	115.5	65.5	88.2
Ssc.28645.1.A1_at, AJ669283	2153.4	1807.4	2627.9	1304.5	1222.5	2798.8	3101.1	2884.2	4191.6	2180.5
Ssc.25102.1.S1_at, CK462383, GAL3ST1	89.1	134.3	130.9	95.1	99.3	134.2	147.4	130.8	367.6	128.2
Ssc.29909.1.A1_at, CO939484, FBXO22	86.8	169.6	40.6	250.1	378.4	144.3	120.2	93.5	71.1	181.7
Ssc.28256.1.A1_at, CO988952, RPL38	567.7	435.8	655.4	825.4	630.8	1675.2	1344.3	677.0	1351.4	550.3
Ssc.13657.1.A1_at, CF180485	50.3	86.6	44.1	74.7	93.0	49.0	34.3	60.8	46.2	21.2
Ssc.11875.1.A1_at, BQ603962, CDCP2	327.2	363.0	222.4	545.4	365.8	149.4	256.3	327.8	105.6	193.1
Ssc.11163.1.S1_at, BI403478, SP140	864.8	993.8	878.7	1392.5	1118.5	556.2	522.1	920.3	365.0	1027.9
Ssc.30827.1.S1_at, CO990980, TBC1D1	619.5	534.9	660.6	429.2	491.8	960.8	536.5	1119.7	750.0	971.3
Ssc.4942.2.S1_at, AW435924, ABHD14B	619.2	688.3	445.7	938.6	866.8	400.2	268.6	590.2	275.1	502.5
Ssc.13104.1.S1_at, BQ604281, NUDT13	123.8	166.2	141.7	223.6	177.3	66.3	108.4	181.5	76.5	117.5
Ssc.31023.1.A1_at, CO942956, RWDD3	436.6	351.5	247.3	528.7	346.2	252.0	141.2	329.8	123.1	271.4
Ssc.25180.1.S1_at, BF444459, DUSP22	688.9	537.0	505.4	639.2	622.9	410.5	270.3	523.4	270.0	504.8
Ssc.23003.1.S1_a_at, CK464707, LRRN2	514.6	481.9	352.7	430.9	519.2	287.6	352.6	248.0	364.7	165.0
Ssc.29973.1.S1_at, BX919432, PHF17	870.3	824.2	723.0	1495.0	957.9	341.1	452.8	927.1	340.2	731.2
Ssc.10247.1.S1_at, CK459862, RFTN2	1826.2	2663.1	1636.5	3787.8	3135.0	1447.5	1120.3	1602.7	585.2	1463.6
Ssc.3902.1.S1_at, BG383587	655.1	460.9	786.7	336.5	390.9	801.7	686.1	867.9	1145.0	655.5
Ssc.7540.1.A1_at, BQ599171, ACMSD	228.8	144.5	138.3	240.1	80.0	57.1	90.9	82.3	95.8	51.4
Ssc.5365.1.S1_at, BI184337	734.0	627.5	863.5	473.2	473.8	668.9	1042.8	1168.7	1235.1	656.9
Ssc.22205.1.A1_at, CF789604, RWDD3	46.2	32.0	30.5	49.3	28.6	24.1	13.9	48.9	18.0	15.2
Ssc.18444.1.S1_at, BG384321, GARS	4564.7	3927.3	4606.5	2516.6	3394.8	4715.0	7471.5	5592.7	9401.9	4342.8
Ssc.4656.1.S1_at, BX922427, CIRH1A	2172.2	1793.9	2247.1	1206.3	1224.7	2232.4	3038.7	2256.8	3917.6	2048.3
Ssc.5480.1.S1_at, BF711106, IRF5	413.3	274.4	274.3	571.8	720.5	234.7	196.2	274.4	148.5	211.8
Ssc.18594.1.S1_at, CF367157, MTDH	627.7	463.7	457.3	230.9	385.9	708.8	636.2	703.5	640.3	561.0
Ssc.21324.1.S1_at, BI340384, MTCP1	158.4	147.4	115.0	241.2	182.7	49.5	89.8	69.6	75.5	136.2
Ssc.8882.1.A1_at, BF708549, KIAA1324	4091.7	3999.6	2113.5	2630.9	3958.3	1659.6	2552.1	2450.8	1872.2	2422.5
Ssc.19980.1.S1_at, BX675506, ADAM28	133.1	161.0	102.4	200.3	276.2	79.6	66.8	92.3	39.5	89.4
Ssc.1257.1.S1_a_at, BI186326, PIK3IP1	1028.2	830.9	326.6	1078.4	814.1	511.4	464.4	561.1	344.9	681.6
Ssc.19455.1.S1_at, CF360719, MGLL	4180.2	3346.1	4686.0	1735.1	2319.5	5847.1	6632.4	4435.8	7923.2	6656.7
Ssc.18746.1.S1_at, CF790887	2960.9	2917.2	2029.8	3294.6	2748.6	1687.7	1405.7	2259.9	1381.4	2540.8
Ssc.2012.1.A1_at, BQ599705, FRMD3	1856.1	2361.2	1802.2	3743.2	2032.6	1625.3	897.1	1953.8	1297.5	1765.1
Ssc.15424.1.S1_at, CA779516, EDIL3	148.3	131.8	119.3	94.4	206.5	58.3	89.1	94.9	66.5	131.2
Ssc.26371.1.S1_at, CN162682, METTL11A	337.5	338.2	401.7	190.0	285.6	407.7	603.4	396.8	515.4	408.6
Ssc.5868.1.S1_at, BI184030	127.2	176.7	232.2	250.8	246.6	153.3	135.6	115.5	95.4	171.9
Ssc.24415.1.A1_at, CK461013, TUBB6	3181.0	2668.1	3000.1	1479.4	1678.2	4419.2	3339.6	4333.2	6399.3	4678.1
Ssc.6119.1.A1_at, CN166734, RAB18	806.4	2199.2	634.3	711.2	718.3	2195.0	2334.2	548.6	3254.3	2463.6
Ssc.23265.1.A1_at, CF362275, ZNF294	93.1	68.9	77.4	77.3	87.4	127.8	142.1	88.0	180.3	135.3
Ssc.8347.1.A1_at, CK465810, ITGAE	360.9	418.1	340.7	439.4	571.9	328.4	225.3	298.8	201.5	351.0
Ssc.8620.1.A1_at, BQ603431, CLEC1A	535.7	636.2	488.9	1236.2	1278.3	201.9	394.7	418.3	291.7	525.8
Ssc.2804.2.A1_at, CO941583, CYB561D2	367.9	350.0	408.5	451.1	515.8	295.5	198.3	380.2	168.8	331.8
Ssc.1967.1.A1_at, CF790817, PHF21A	1395.8	1051.1	706.0	858.2	953.5	1069.2	1771.9	773.5	2861.1	1349.1
Ssc.22880.1.A1_at, BX669739, RALGPS2	183.0	146.0	112.1	210.9	115.7	191.8	187.3	340.7	306.9	134.5
Ssc.6727.1.S1_at, BF704252, IPO5	2201.3	1786.5	2510.5	1300.0	1270.8	2622.8	3513.8	3032.1	3698.6	2121.3
Ssc.15720.1.A1_at, CN160994, CNDP2	1722.0	1521.5	1863.9	2396.6	3149.7	1234.5	1121.9	1775.5	1179.4	1350.7
Ssc.24580.1.A1_at, CK464772, LAMB1	178.9	85.3	126.7	124.9	113.4	237.9	267.6	218.5	279.5	184.8
Ssc.2585.1.A1_at, BI403219, FOXF1	164.9	143.2	69.1	330.5	65.1	31.3	84.4	69.0	17.8	67.0
Ssc.27729.1.S1_at, BE032389, NOC3L	79.2	77.4	87.0	57.8	49.1	121.3	145.4	63.0	188.8	122.5
Ssc.3994.1.S1_at, BF713387, PDCD2L	132.3	129.5	185.8	110.5	105.8	205.5	204.2	168.1	302.0	201.9
Ssc.10642.1.S1_at, CN162548	78.8	97.9	58.1	139.5	101.8	59.3	27.2	64.0	18.5	47.1
Ssc.30893.1.A1_at, CK461249, GULP1	399.7	663.2	524.0	808.9	518.0	384.8	468.4	319.1	256.4	433.9
Ssc.5041.1.A1_at, CN154405	2024.4	1694.3	2235.8	953.6	1279.2	1971.0	2589.2	2186.0	3957.2	1875.3
Ssc.8646.1.A1_at, BQ603398	147.7	124.5	125.0	176.0	145.7	77.7	99.9	116.7	61.2	117.9
Ssc.10681.1.A1_at, BQ597652, PDZRN4	84.1	125.6	273.8	98.3	151.9	169.0	72.7	83.5	24.7	104.6
Ssc.13358.1.A1_at, BI405073, AGBL3	196.4	144.3	63.3	296.7	158.2	67.1	56.2	123.8	51.9	94.5
Ssc.21987.1.A1_at, BM083178, IFRD1	1889.7	1768.9	1726.4	1195.1	1194.5	2672.5	2654.9	2356.4	2947.9	1776.3
Ssc.21092.1.S1_at, BX676574, TMTC2	88.0	86.1	46.2	159.7	176.7	159.0	36.7	37.3	50.5	51.3
Ssc.24728.2.S1_a_at, CK466412, UCK2	3110.1	2198.7	3575.2	2135.0	1607.4	4186.1	5324.1	3530.8	7024.5	3204.0
Ssc.23797.1.S1_at, NM_213779.1	221.0	146.7	239.6	368.3	267.1	85.4	85.7	217.1	221.3	160.4
Ssc.10946.2.A1_at, BQ602339, NAT13	323.0	477.4	403.4	131.3	370.6	711.6	841.9	267.0	716.8	460.8
Ssc.6670.1.A1_at, BQ599672, SLC39A6	952.2	1715.0	2028.2	1090.3	1044.6	2469.2	2698.3	1658.4	3545.8	2111.7

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
62.4	56.0	37.5	65.1	56.7	34.2	213.3	119.7	52.0	27.0	74.7	13.0	0.243709955	0.434352718
47.7	41.0	31.8	49.0	36.5	33.4	183.4	92.0	39.9	79.1	23.9	7.3	0.217509812	0.433789954
1656.3	976.5	1616.7	632.4	1085.2	1919.2	1823.1	3031.2	1314.4	588.8	733.3	491.1	0.720944817	0.433612427
83.0	78.0	79.5	77.9	75.6	78.1	109.7	181.6	78.7	21.2	104.2	2.5	0.716997752	0.433182853
65.6	93.6	31.0	30.1	39.8	57.4	185.1	122.2	52.9	134.5	43.2	24.5	0.285881505	0.433175071
398.5	402.5	319.7	970.5	351.7	464.0	623.0	1119.6	484.5	141.6	482.9	243.1	0.777636887	0.432713491
20.2	21.1	13.3	19.1	15.9	20.2	69.7	42.3	18.3	21.7	15.1	3.0	0.262403212	0.432624113
107.3	118.2	50.4	69.8	115.6	74.4	364.8	206.4	89.3	116.5	87.8	28.2	0.244772819	0.432490473
274.9	262.8	238.5	402.4	148.4	431.7	1049.7	678.3	293.1	217.3	282.1	106.1	0.279249154	0.432134257
486.2	327.8	366.9	341.0	306.7	420.8	547.2	867.7	374.9	93.9	227.2	67.2	0.685124269	0.432081691
148.3	238.9	126.5	245.2	221.0	75.8	711.7	407.3	176.0	197.1	140.8	69.3	0.247218007	0.43196995
45.6	60.0	51.1	57.8	38.1	32.5	166.5	110.0	47.5	38.1	45.3	10.9	0.285351109	0.431812674
62.3	143.4	86.9	113.4	68.4	103.8	382.1	223.5	96.4	105.9	88.4	30.3	0.252229144	0.431170768
157.0	240.5	137.3	161.6	199.4	127.2	598.7	395.8	170.5	75.6	122.4	42.4	0.284793212	0.430773118
103.6	153.5	112.7	84.5	101.3	176.6	459.9	283.6	122.0	69.5	81.7	35.3	0.26537062	0.430331241
296.1	298.8	222.5	253.7	250.6	118.9	974.1	558.5	240.1	303.3	260.7	66.1	0.246488995	0.429916917
577.3	628.2	416.4	723.0	474.7	387.2	2609.7	1243.9	534.5	898.3	408.5	130.7	0.204798471	0.429683941
424.6	435.7	443.9	246.4	290.9	301.5	526.0	831.2	357.2	189.1	195.3	87.2	0.678998264	0.429679355
32.5	55.5	28.4	31.9	24.8	20.9	166.3	75.5	32.3	67.2	20.1	12.2	0.194380987	0.428256071
512.7	408.8	485.6	289.6	302.9	452.7	634.4	954.5	408.7	169.0	275.0	93.9	0.644257041	0.428208728
10.5	9.2	7.8	6.5	10.4	17.3	37.3	24.0	10.3	9.7	14.5	3.8	0.275544837	0.428115459
3325.9	2219.5	3245.3	2064.2	2299.7	3025.4	3802.0	6304.8	2696.7	875.0	2111.7	564.0	0.709279551	0.427717806
1579.0	900.8	1325.5	842.1	840.9	1437.3	1728.8	2698.8	1154.3	499.1	780.6	331.6	0.667653841	0.427702599
114.2	54.2	69.7	136.8	86.6	84.9	450.9	213.1	91.1	194.3	46.6	30.0	0.201984356	0.427302302
344.6	214.3	367.5	169.1	253.5	315.6	433.1	650.0	277.4	143.6	60.3	77.9	0.640575695	0.42684678
45.9	46.2	32.3	34.6	37.4	19.0	168.9	84.1	35.9	47.2	32.5	10.1	0.21250148	0.426771279
882.9	1213.3	1206.7	1007.8	749.0	545.7	3358.8	2191.4	934.2	920.3	398.6	262.8	0.278144972	0.42631025
51.3	12.7	21.5	52.6	30.5	19.4	174.6	73.5	31.3	67.3	21.5	17.0	0.179457808	0.426187885
234.5	261.4	222.0	307.4	175.6	107.9	815.6	512.7	218.1	297.3	123.9	69.4	0.267438249	0.425476581
3419.9	2014.0	2817.0	2109.5	2927.8	2789.6	3253.4	6299.0	2679.6	1234.6	1279.9	530.8	0.823645972	0.425403448
865.4	1219.4	700.9	817.0	663.3	468.8	2790.2	1855.1	789.1	468.9	521.6	252.2	0.282821187	0.425385873
1172.7	533.2	827.7	758.6	292.4	260.1	2359.1	1507.8	640.8	804.0	417.2	349.2	0.271626552	0.424990273
35.6	53.4	36.1	30.6	37.9	30.5	140.1	88.0	37.4	42.0	28.5	8.4	0.266671427	0.424431818
250.2	163.1	193.0	123.7	120.4	333.0	310.6	466.4	197.2	79.0	90.6	82.1	0.635007512	0.42290264
65.3	85.2	54.8	49.4	27.4	58.7	206.7	134.3	56.8	53.4	30.2	19.0	0.274794388	0.422807801
2572.5	1744.0	2251.7	1688.7	1907.2	1590.4	2401.4	4633.9	1959.1	776.3	1110.2	379.4	0.815822423	0.42277386
474.6	1064.4	1182.1	1381.5	307.5	1063.7	1013.9	2159.1	912.3	665.4	989.7	423.4	0.899810628	0.42252934
53.3	52.0	83.4	41.3	58.0	53.1	80.8	134.7	56.9	9.5	33.0	14.1	0.703414996	0.422048998
160.4	133.1	113.0	123.1	103.6	77.4	426.2	281.0	118.4	90.9	65.0	28.0	0.277882059	0.421470937
139.6	235.6	121.0	196.9	119.6	112.8	835.1	366.5	154.3	389.3	124.0	50.4	0.184717266	0.420896093
102.0	114.3	118.6	117.9	87.1	154.0	418.7	274.9	115.7	66.9	89.3	22.3	0.276238475	0.420667831
749.5	879.7	669.2	492.7	487.9	668.0	992.9	1565.0	657.8	258.7	812.6	151.0	0.662524003	0.420351532
69.9	147.0	108.4	108.7	75.6	75.6	153.5	232.2	97.5	42.9	87.4	29.7	0.635230776	0.419967849
1693.9	1067.4	1383.1	731.2	1219.4	1452.7	1813.8	2997.7	1258.0	546.6	645.6	334.3	0.693536294	0.41963559
743.7	460.4	515.4	625.1	405.3	603.6	2130.7	1332.4	558.9	655.4	261.7	123.1	0.262311059	0.419481137
64.7	84.6	108.3	68.7	155.2	115.5	125.8	237.7	99.5	34.0	38.1	34.1	0.790686586	0.41866532
28.9	15.5	23.1	10.9	18.2	38.5	154.6	53.9	22.5	107.8	28.0	10.0	0.145682367	0.417748918
91.8	52.0	51.1	48.7	31.6	46.0	70.1	128.2	53.5	15.9	45.6	20.2	0.763670946	0.417576703
113.8	89.1	85.7	67.4	68.0	117.7	132.8	216.3	90.3	31.8	50.3	21.7	0.679946779	0.4173215
28.3	18.6	19.5	25.9	6.6	9.2	95.2	43.2	18.0	30.2	19.8	8.7	0.18921095	0.416859479
153.6	159.3	100.9	212.3	222.0	82.5	582.8	372.5	155.1	157.1	85.8	56.5	0.266147299	0.416353484
1418.3	961.8	1179.2	819.5	866.5	1037.1	1637.5	2515.7	1047.1	526.1	851.3	222.3	0.639445645	0.416206232
47.2	33.6	35.8	41.4	40.0	38.4	143.8	94.7	39.4	21.1	24.8	4.7	0.274029768	0.416138572
40.2	29.7	52.7	33.4	37.0	33.8	146.7	90.9	37.8	75.6	52.6	8.1	0.257598473	0.415841584
29.5	53.5	33.5	32.1	35.4	12.1	171.8	78.7	32.7	85.0	30.2	13.2	0.190262739	0.415290131
1542.1	762.5	1415.5	230.3	369.0	1862.7	1554.9	2481.6	1030.4	334.2	446.4	671.2	0.662638592	0.415195841
8.3	50.9	22.4	24.0	33.4	27.5	111.3	67.0	27.8	54.9	51.9	14.1	0.249236573	0.414426523
2521.4	1277.5	2133.9	1020.1	1284.7	3325.6	2525.3	4653.9	1927.2	797.8	1553.3	895.4	0.763162897	0.4141043
71.9	46.9	42.0	53.8	58.1	109.4	248.5	154.0	63.7	80.5	66.9	24.7	0.256229715	0.41358185
376.3	199.2	224.1	141.5	178.8	365.7	341.1	599.6	247.6	130.1	231.8	99.4	0.725801724	0.412928188
1428.4	905.6	848.0	810.7	810.3	1370.4	1366.1	2496.7	1028.9	477.2	705.9	289.7	0.753188001	0.412107278

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.27201.1.S1_a_at, NM_001001617.1, CCRL2	66.3	61.8	73.7	115.3	112.7	64.3	45.3	63.1	28.9	50.2
Ssc.10765.1.A1_at, CD015907, PTBP2	357.5	430.9	286.2	509.9	457.9	494.2	626.7	428.7	1001.7	515.0
Ssc.76.3.S1_a_at, CF368013, TGFB1	2614.4	1635.3	3212.3	936.2	1142.9	4007.7	3850.2	2038.6	4705.5	3237.7
Ssc.10434.1.S1_at, CF367863, FZD8	2203.6	2444.0	1720.0	2709.3	4191.8	1106.2	1913.4	2109.8	1632.7	1626.2
Ssc.3250.1.S1_at, AW353790	329.0	305.1	320.8	574.6	504.2	284.6	225.2	196.1	187.9	262.6
Ssc.1864.1.A1_at, BF710490, TNFRSF12A	1167.0	1210.1	1452.7	531.0	498.1	1365.1	1711.8	1461.7	2213.4	1339.1
Ssc.8352.1.A1_at, BF713095, NAP1L3	127.7	145.5	97.0	205.8	157.1	45.2	67.9	136.6	29.3	136.7
Ssc.15888.1.S1_at, NM_213805.1, OLR1	3528.3	1932.0	3828.3	396.0	1603.2	5248.5	4894.2	1511.6	5257.4	3075.3
Ssc.29738.1.A1_at, CO944155, RHOT1	835.7	635.8	466.7	731.7	808.4	369.5	349.5	425.6	328.1	791.4
Ssc.9215.1.A1_at, BF709901	272.5	751.1	518.2	258.3	231.6	479.5	326.7	162.9	204.8	117.9
Ssc.30506.1.A1_at, CO992869, MAP3K5	881.0	891.9	469.1	1320.1	1374.1	469.3	794.8	708.4	264.2	657.7
Ssc.21782.1.S1_at, CN166950, ZNF658	87.5	45.0	41.0	180.2	82.7	53.4	31.7	64.5	29.5	37.9
Ssc.2960.1.A1_at, CF788009, ATP11A	1697.1	2726.9	3718.3	1889.6	2419.9	4736.2	2939.5	1937.9	4940.8	4262.6
Ssc.6277.1.A1_at, CF365455, PCNT	608.6	527.7	491.8	690.3	794.3	343.8	332.9	389.8	265.4	476.3
Ssc.12817.1.S1_at, BX670344, PLXNA2	1532.2	1407.2	1669.4	876.5	814.9	1524.2	2417.8	1346.6	3475.6	1434.6
Ssc.21909.1.S1_at, BX666832, EPHA4	685.5	854.4	533.5	1720.7	1703.3	217.4	850.3	710.5	481.3	434.2
Ssc.3879.1.S1_at, AJ747527, PLXNC1	443.8	310.9	392.1	569.8	980.2	206.0	117.1	474.9	164.5	128.5
Ssc.20883.1.S1_at, CO943860, SELENBP1	1189.2	1896.1	867.7	2477.6	3504.3	817.7	318.5	1030.5	275.7	1246.7
Ssc.18317.1.A1_at, CF179802, SOS2	217.7	188.5	286.2	509.0	300.1	169.0	174.6	291.9	111.1	218.5
SscAffx.8.1.S1_s_at, NM_001005154.1, MYC	1007.5	1555.9	1589.5	1376.4	1513.4	1237.7	3547.8	1879.5	3967.4	2076.8
Ssc.25253.2.A1_at, CF180830, GRM7	158.5	505.3	320.1	222.3	135.9	255.8	200.2	138.9	111.6	94.8
Ssc.11810.1.A1_at, CF176441	466.9	365.3	378.5	322.7	391.2	260.0	303.9	205.2	155.1	234.6
Ssc.10819.1.S1_at, CK461153, NIT2	618.5	690.7	453.5	902.4	944.4	436.7	289.0	536.5	212.8	535.7
Ssc.29913.1.A1_at, CO939566, LUZP2	1130.8	656.6	811.5	1685.7	1146.4	430.8	518.7	1174.0	420.8	414.7
Ssc.924.3.A1_at, BF710863, THBS1	1057.7	3097.5	2029.4	450.4	2755.2	4236.1	3857.5	1574.5	3275.2	2641.3
Ssc.13675.1.A1_at, BQ601824, MUC4	198.8	173.3	144.6	269.5	242.0	100.6	120.8	149.9	87.8	142.6
Ssc.17625.1.A1_at, CF365795, C1orf57	297.4	454.4	418.2	333.1	235.2	201.2	164.3	300.0	85.5	274.3
Ssc.30928.1.A1_at, CO955506, IPO5	994.3	953.0	1167.6	860.7	687.7	1388.2	1534.7	1258.9	1713.3	1132.7
Ssc.2910.1.A1_at, BI185420, ZNF655	248.3	229.9	193.7	355.6	439.3	173.9	159.0	220.1	154.5	175.3
Ssc.14209.1.A1_at, BQ600790, EFNA5	305.0	464.3	356.9	853.3	838.0	118.8	210.2	621.2	162.4	268.4
Ssc.2680.1.S1_at, CK462390, LRRC59	2901.0	2773.2	2865.2	1344.9	1665.3	4268.0	4468.1	2871.6	6280.3	2809.6
Ssc.26060.1.A1_at, AJ686121	401.1	446.0	368.3	347.1	988.3	426.3	214.1	279.3	142.1	184.6
Ssc.13322.1.A1_at, BI404618, C10orf122	1481.1	1719.4	1247.5	2455.5	1922.3	690.4	939.4	1323.9	704.4	1520.2
Ssc.28479.1.S1_at, CB097331, TMOD1	1115.8	953.9	823.9	1303.2	877.0	782.5	568.5	835.8	378.2	599.0
Ssc.13156.1.A1_at, BQ604560, C8orf4	215.1	264.6	431.1	330.3	419.0	573.9	382.4	1429.0	1553.5	740.4
Ssc.19304.1.A1_at, BE032545, DYNC2H1	1045.9	606.6	1434.7	566.8	326.1	1982.1	2509.5	3128.5	2327.7	841.9
Ssc.13637.1.A1_at, BQ602979, PRKCA	1061.9	822.1	590.1	210.4	468.5	1171.5	1782.3	673.2	1411.8	1274.4
Ssc.657.1.A1_at, NM_214214.1, CCL2	1903.7	1522.1	3253.8	1722.1	795.3	3268.9	7267.1	7517.9	7749.6	2142.2
Ssc.7207.3.A1_at, BQ598212, SP100	158.5	182.5	64.7	209.9	123.2	26.3	82.7	52.6	33.8	100.3
Ssc.3734.1.S1_at, BE231712, DDX31	128.1	139.8	126.4	75.6	104.8	110.4	218.9	136.2	302.6	146.1
Ssc.30377.1.A1_at, AW486597, TBC1D22A	243.1	237.9	181.3	216.0	144.3	252.8	274.3	306.9	427.2	306.2
Ssc.4283.1.S1_at, CK462616, BIN2	114.3	142.0	88.2	206.8	312.4	85.1	65.9	35.4	83.2	63.3
Ssc.9035.1.A1_at, BQ602007, PRSS23	271.3	255.5	280.9	143.5	338.6	436.8	254.0	606.1	556.2	1031.2
Ssc.22509.1.S1_at, CK449586, C1orf163	208.1	176.3	219.4	179.0	171.9	169.1	359.0	273.2	401.2	239.2
Ssc.8549.1.A1_at, BF704147, GUCY1A3	454.3	709.2	341.8	613.6	1221.9	383.9	362.4	432.4	265.1	453.8
Ssc.18444.3.S1_at, BP158015, GARS	459.0	577.9	573.3	77.0	383.5	810.5	1142.1	329.4	1448.9	546.8
Ssc.18359.1.S1_at, NM_001001621.1, CCR1	235.0	217.2	399.7	634.9	649.3	127.2	137.4	215.3	148.8	159.4
Ssc.2664.1.S1_at, CK463764, CNTN3	86.3	36.2	35.4	49.0	138.5	26.4	21.0	22.3	37.5	40.3
Ssc.30397.1.A1_at, CO990793, CCDC146	267.2	58.1	136.0	232.0	278.2	137.3	66.6	49.6	37.1	102.2
Ssc.13903.1.S1_at, CF795324, SMS	519.7	464.6	556.4	341.7	316.0	574.3	717.5	686.9	927.9	421.1
Ssc.30972.1.S1_at, AW478144, FAM60A	157.1	168.8	130.6	64.2	128.8	171.4	216.8	95.3	472.5	143.4
Ssc.5488.1.S1_at, BF193197, TCTN3	3911.3	5786.6	5374.8	4288.1	4712.3	7033.1	6754.8	7001.6	8372.9	9001.8
Ssc.24741.1.A1_at, CK464409, UTRN	345.8	423.5	507.2	475.3	435.1	728.9	681.7	546.5	804.3	522.2
Ssc.8010.1.S1_at, BF710104, C6orf66	472.2	416.9	552.7	343.9	294.0	520.9	825.0	436.9	1006.1	460.8
Ssc.4242.1.A1_at, CO953825, DUSP23	253.3	222.2	286.3	316.6	355.7	176.8	167.2	255.0	112.2	235.8
Ssc.4217.1.S1_at, NM_001001537.1, ITIH4	293.5	281.3	220.0	463.9	340.7	288.2	85.8	162.6	94.0	183.9
Ssc.5856.1.A1_at, BQ603201, SENP8	533.5	481.1	528.1	797.3	752.5	332.5	374.2	402.8	321.2	528.7
Ssc.20801.1.S1_at, BX676239, FBXO22	1313.0	1662.2	950.2	1968.3	3238.3	1050.9	829.9	1230.6	603.7	1426.6
Ssc.1864.1.A1_a_at, BF710490, TNFRSF12A	1881.6	1240.3	2093.6	582.1	540.1	1391.9	2554.4	2308.7	2947.9	1436.1
Ssc.15739.1.S1_at, NM_214083.1, IL2RG	105.4	105.6	119.1	231.4	256.1	49.1	91.8	113.2	128.4	138.3
Ssc.8374.1.A1_at, BP173076, C7orf10	252.1	235.8	223.5	186.4	195.8	292.5	322.9	619.0	341.3	232.4

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
28.3	13.1	17.7	25.7	9.2	30.0	86.0	50.4	20.7	26.0	14.5	8.6	0.240421902	0.410378607
225.6	297.6	224.5	188.3	271.7	301.5	408.5	613.3	251.5	87.7	228.6	45.7	0.615778822	0.410157736
2161.5	1196.6	1873.2	889.6	1346.2	1306.8	1908.2	3567.9	1462.3	975.2	1001.9	467.8	0.766324987	0.409849007
664.8	820.0	737.6	852.7	508.4	536.6	2653.7	1677.7	686.7	933.7	378.7	143.3	0.258760592	0.40931019
160.5	82.9	67.1	100.3	69.1	87.9	406.7	231.3	94.6	123.9	41.8	34.5	0.232662962	0.409172143
899.7	641.3	651.3	353.9	528.0	898.4	971.8	1618.2	662.1	431.5	363.8	212.5	0.681327049	0.409153267
31.0	22.0	44.7	40.8	15.7	49.8	146.6	83.1	34.0	40.1	50.7	13.4	0.231891966	0.408948761
1320.6	646.1	1029.0	176.4	823.0	5770.7	2257.6	3997.4	1627.6	1421.4	1657.3	2065.7	0.720970133	0.407172996
150.8	182.9	217.2	174.6	182.8	197.9	695.7	452.8	184.4	149.7	192.7	22.3	0.265024102	0.407152216
119.8	111.4	129.7	79.1	100.7	88.0	406.3	258.4	104.8	224.6	146.0	19.2	0.257871077	0.405571038
339.3	261.3	165.4	259.6	125.7	256.9	987.2	578.9	234.7	370.6	212.5	76.7	0.237733479	0.405438087
7.7	24.5	14.1	21.2	10.1	27.9	87.3	43.4	17.6	56.1	15.0	8.2	0.201458906	0.405145929
1924.7	1596.4	1555.9	1275.9	1351.2	1443.7	2490.4	3763.4	1524.6	799.8	1283.8	230.1	0.612214031	0.405121256
115.3	199.0	127.0	198.3	132.8	105.3	622.5	361.6	146.3	122.9	78.0	41.7	0.234978208	0.404499871
1052.6	739.1	882.4	721.5	655.2	895.7	1260.0	2039.8	824.4	390.0	910.6	146.3	0.654278171	0.404173367
228.5	184.7	231.1	413.2	140.3	107.5	1099.5	538.7	217.6	570.6	247.0	107.5	0.197866264	0.4038126
208.9	23.4	40.9	169.7	44.4	41.2	539.4	218.2	88.1	263.8	147.6	79.7	0.163310838	0.403681638
271.0	243.5	220.5	653.1	203.2	195.5	1987.0	737.8	297.8	1053.6	430.2	176.2	0.149875691	0.403621479
77.6	107.6	77.9	79.9	60.1	63.9	300.3	193.0	77.8	125.6	67.2	16.7	0.259185259	0.403239733
1127.3	1145.3	1179.6	327.9	655.9	1708.2	1408.5	2541.8	1024.0	238.4	1161.9	477.0	0.727017574	0.402870886
56.9	72.3	51.9	81.5	80.5	44.2	268.4	160.3	64.6	150.5	66.8	15.7	0.240481335	0.402782978
84.9	122.1	104.9	85.7	79.1	83.2	384.9	231.8	93.3	52.6	56.1	16.7	0.242431328	0.402643539
131.1	206.2	109.7	231.2	177.2	113.6	721.9	402.1	161.5	203.6	146.4	51.0	0.223715196	0.401601432
169.0	405.2	293.1	189.3	134.7	233.3	1086.2	591.8	237.4	395.3	328.2	98.8	0.218590806	0.401205362
1203.3	1510.7	1085.2	779.3	1075.3	1844.7	1878.0	3116.9	1249.8	1117.0	1052.5	375.0	0.66545441	0.400956714
32.0	83.7	28.2	45.6	41.0	58.8	205.6	120.3	48.2	50.5	26.5	20.5	0.234471244	0.400670323
82.0	104.5	68.1	58.5	65.2	114.6	347.7	205.1	82.2	89.1	86.3	22.8	0.23629408	0.400614454
738.2	486.5	586.9	312.4	489.1	756.4	932.7	1405.6	561.6	176.5	227.8	169.0	0.602130823	0.399544191
74.5	61.3	53.5	104.4	59.9	69.3	293.4	176.6	70.5	101.4	26.0	18.2	0.240262249	0.399203293
125.5	77.0	86.7	140.2	143.9	87.2	563.5	276.2	110.1	264.0	200.7	29.8	0.195356403	0.398563843
2209.1	1208.3	1844.1	1094.3	1425.7	2098.8	2309.9	4139.5	1646.7	744.8	1421.6	470.3	0.712889047	0.397803771
143.5	65.7	82.8	123.7	104.0	73.7	510.2	249.3	98.9	269.9	110.8	30.4	0.19386075	0.396742619
479.6	706.6	356.0	377.9	312.9	226.9	1765.2	1035.7	410.0	461.5	372.8	167.2	0.23226412	0.395866726
246.8	360.0	189.5	252.1	122.4	331.8	1014.8	632.8	250.4	195.3	182.8	88.0	0.246790703	0.395754319
242.8	85.9	283.6	15.8	154.7	1438.8	332.0	935.8	370.3	94.3	524.5	532.6	1.115193864	0.395651678
960.1	291.4	1225.3	68.8	843.8	1727.9	796.0	2157.9	852.9	441.5	845.2	607.6	1.071434554	0.395230328
792.2	507.5	551.5	210.2	428.2	504.5	630.6	1262.6	499.0	326.8	402.5	188.3	0.791336293	0.3952169
2721.7	715.8	2352.6	279.6	2161.4	5022.2	1839.4	5589.1	2208.9	895.7	2667.8	1682.4	1.200871661	0.395209877
36.9	12.5	21.5	19.6	20.4	29.2	147.8	59.1	23.4	56.3	31.7	8.5	0.15802653	0.394825837
100.0	66.6	84.0	40.2	65.8	75.6	114.9	182.8	72.0	25.4	78.1	20.1	0.626703787	0.393969226
148.5	126.0	147.1	107.6	107.8	102.3	204.5	313.5	123.2	41.5	67.5	20.7	0.602467566	0.393060695
35.5	21.9	22.1	34.0	22.0	21.5	172.7	66.6	26.2	89.7	20.0	6.7	0.151480066	0.393010914
243.8	105.7	188.8	186.1	274.3	357.5	258.0	576.9	226.0	71.3	287.9	86.5	0.876234041	0.391833952
139.7	68.9	124.8	73.6	87.9	182.7	190.9	288.3	112.9	21.4	93.0	44.4	0.591459795	0.391667245
135.6	105.4	107.8	211.5	99.4	231.6	668.2	379.5	148.6	340.4	73.7	58.3	0.222326988	0.391415472
450.9	257.7	315.7	263.9	265.1	455.8	414.1	855.5	334.9	205.4	449.5	94.1	0.808543005	0.391390233
103.4	43.4	65.4	80.0	47.4	30.2	427.2	157.6	61.6	208.7	34.4	26.9	0.14426603	0.391024828
16.0	5.9	9.1	14.7	5.9	17.6	69.1	29.5	11.5	44.0	8.9	5.2	0.166956186	0.390960452
39.6	29.7	12.1	39.8	39.8	23.2	194.3	78.6	30.7	94.5	41.0	11.4	0.158003088	0.390784114
272.8	205.8	271.6	239.3	239.8	330.8	439.7	665.5	260.0	106.7	187.1	42.6	0.591377062	0.390685258
89.2	94.5	65.2	55.8	79.8	130.4	129.9	219.9	85.8	40.5	147.9	26.2	0.660636387	0.390288642
3024.9	2907.0	3234.0	2740.4	2217.4	3748.8	4814.6	7632.8	2978.8	768.5	993.8	510.3	0.618688495	0.390254479
268.5	215.6	210.1	313.3	291.0	235.6	437.4	656.7	255.7	61.0	120.3	42.0	0.584579389	0.389333861
307.1	197.4	252.5	145.0	174.9	441.3	415.9	649.9	253.0	102.4	252.6	108.8	0.608340947	0.389317988
65.5	59.3	64.9	121.3	47.0	84.3	286.8	189.4	73.7	52.3	57.2	26.2	0.25701369	0.389211545
69.3	54.6	48.8	57.2	74.8	75.5	319.9	162.9	63.4	91.3	81.9	11.3	0.198095119	0.388991201
134.6	165.4	119.7	229.2	108.5	156.6	618.5	391.9	152.3	145.1	83.2	43.4	0.246294799	0.388724439
415.4	581.3	290.3	436.1	242.7	428.1	1826.4	1028.3	399.0	876.3	323.9	120.0	0.218453424	0.38798776
1274.1	713.0	899.4	398.7	794.9	873.1	1267.5	2127.8	825.5	717.5	690.5	284.5	0.651287796	0.38797506
55.9	22.2	17.1	65.8	24.4	56.8	163.5	104.2	40.4	74.0	35.4	21.4	0.246860731	0.387544803
169.6	133.9	140.7	97.3	146.4	152.3	218.7	361.6	140.0	27.4	149.7	24.2	0.640240185	0.387238906

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.17100.1.S1_at, BF710549, S100A8	42.7	43.0	119.4	51.5	57.5	121.9	66.4	83.7	73.2	198.1
Ssc.12026.1.A1_at, CK462144, CASP7	2810.9	3516.5	3706.6	1380.4	3343.3	5326.5	7135.4	4337.1	6345.9	5524.9
Ssc.26879.2.S1_at, CN161783, TNFSF13	279.1	397.7	209.9	355.9	374.3	156.7	168.7	214.6	109.5	143.6
Ssc.11798.1.A1_at, BI184730, GNB1L	1586.0	1317.3	2121.7	855.4	1300.8	1977.6	2673.1	1861.6	2960.0	2201.5
Ssc.12872.1.A1_at, BI404002, C13orf18	1499.6	1731.0	1100.8	1899.1	1879.8	543.1	841.4	1007.5	712.7	1169.6
Ssc.508.1.S1_at, AF148221.1, FCER1G	881.0	770.8	745.1	1822.0	1801.1	548.0	350.0	758.0	358.7	562.9
Ssc.11734.1.A1_at, BI184240	82.1	90.5	64.4	101.8	207.0	46.4	43.4	75.5	12.3	56.0
Ssc.19276.2.A1_at, CF365859, KCNH1	789.8	564.5	665.8	603.6	433.1	903.6	1587.2	1130.3	2237.5	823.4
Ssc.18671.1.A1_at, CF360581, CSNK2A2	182.3	109.4	124.5	137.7	102.2	240.8	200.1	154.5	362.6	186.0
Ssc.6930.1.A1_at, BQ597658, FRY	2212.8	1754.4	1734.4	2205.9	1526.4	601.8	1476.9	946.8	1331.5	1625.1
Ssc.26732.1.S1_at, CN159136	430.8	370.4	735.7	471.4	422.5	711.6	888.2	930.0	658.6	530.6
Ssc.8710.1.A1_at, BF704230, SLC4A7	652.2	611.3	557.9	395.3	231.4	949.3	1661.7	576.9	2064.5	713.4
Ssc.7493.1.A1_at, CO939368, SIRT1	649.2	732.2	435.3	673.7	880.4	266.0	396.2	381.2	411.7	373.0
Ssc.21194.1.S1_at, CK451828, PTPRR	4374.9	4524.8	3400.2	3310.3	2050.6	1903.2	2782.9	1743.1	1540.2	1918.8
Ssc.27019.1.S1_at, CN165656, CHN2	679.1	824.2	750.8	447.1	1017.8	342.4	445.9	325.3	80.4	343.5
Ssc.14147.1.A1_at, BQ600506, SLC4A5	305.6	191.5	239.8	243.7	156.5	395.2	566.7	234.4	583.9	263.3
Ssc.2459.1.S1_at, CK452493, PAK1IP1	1448.2	724.4	857.6	515.7	631.5	1042.1	1706.4	1078.6	1847.5	707.1
Ssc.24959.1.S1_at, BE013645, NOLC1	1897.2	1870.3	2089.3	1139.3	1135.0	2445.1	3341.9	2109.7	4944.6	1919.8
Ssc.1849.1.A1_at, BI183275, TSEN34	1606.0	1365.0	1543.6	2468.6	2048.3	839.6	1012.6	1679.2	518.2	1219.2
Ssc.30662.1.S1_at, BE233900, CMPK1	254.4	266.8	128.3	287.3	267.0	207.5	79.9	139.1	101.1	202.9
Ssc.18224.1.S1_at, CK464539, UBE4B	142.0	131.3	160.3	150.5	240.2	113.2	78.7	89.6	78.8	124.4
Ssc.2025.1.S1_at, BF701840, SFRS3	4862.3	5245.9	4391.4	3938.1	5524.5	7317.0	6433.0	8195.9	7450.3	7501.0
Ssc.1418.1.S1_at, CF180178, DDX56	329.5	265.0	290.4	157.6	228.7	360.6	366.2	385.1	554.2	299.9
Ssc.12652.1.A1_at, BI403142, HOXA10	1804.2	1324.2	204.8	1799.6	2077.0	229.2	1108.7	740.9	186.7	1489.6
Ssc.30639.1.S1_at, BE012747	345.1	278.5	493.2	304.7	328.1	528.5	448.3	360.4	694.9	601.6
Ssc.30942.1.A1_at, AJ658810, TMEM165	594.4	488.2	581.0	736.6	384.9	550.6	1186.6	1195.3	1620.4	725.6
Ssc.14392.1.A1_at, NM_213852.1, MSMB	688.8	1087.5	2030.3	1334.9	581.5	200.0	91.2	1032.2	184.4	496.4
Ssc.19455.2.S1_at, CN028971, MGLL	682.8	701.0	754.1	239.8	525.7	1182.8	1257.0	747.9	1976.3	1082.0
Ssc.24520.1.A1_at, CK459086, CWF19L2	915.6	1049.9	836.1	1463.2	1213.5	638.7	664.5	773.3	555.0	806.8
Ssc.11857.1.A1_at, BI185370, RPL34	185.3	153.2	168.0	151.8	127.8	203.8	255.1	132.8	470.0	292.9
Ssc.3830.1.A1_at, CN154017, PIGO	550.6	526.8	503.7	828.8	965.2	397.8	465.9	580.4	356.2	415.6
Ssc.13587.2.S1_at, CK466243, ANK3	1337.2	1301.3	716.8	653.5	1343.8	695.6	389.8	523.6	387.7	529.6
Ssc.21239.1.S1_at, BX672979, SLC13A4	286.1	373.4	315.7	251.9	387.8	175.6	214.6	198.9	153.6	247.1
Ssc.30273.1.A1_at, CO989612, RALA	56.6	91.3	45.6	67.4	94.1	103.4	103.7	83.0	146.9	100.6
Ssc.24719.1.S1_at, CK463776, TXNDC10	47.4	74.7	80.3	31.7	68.2	110.4	170.6	62.7	78.3	55.6
Ssc.7576.3.S1_at, CA779332, SFRS1	1769.1	1714.1	1648.9	736.7	1108.9	2263.3	2636.5	2253.9	2450.4	1597.6
Ssc.11877.1.A1_at, BI185607	315.9	324.3	229.2	471.0	431.1	110.7	171.4	140.0	107.6	282.9
Ssc.23881.1.A1_at, CK450548, SMARCAL1	270.2	302.7	342.3	135.4	229.3	417.0	455.7	151.9	837.9	364.7
Ssc.10238.1.A1_at, BI400310, SLC12A1	196.3	297.3	186.2	365.0	180.7	99.2	96.9	141.1	116.6	241.2
Ssc.7225.2.S1_at, BX671906, BAG1	683.1	771.8	771.5	241.1	653.4	1387.8	1180.7	541.5	1087.6	532.7
Ssc.25151.1.S1_at, CK464413, CCDC90A	763.1	641.6	891.6	421.2	387.0	911.7	1079.5	709.9	1197.7	761.8
Ssc.10556.1.S1_at, BF080740, BAZ2B	111.8	122.4	84.3	126.0	195.9	60.4	73.1	39.9	47.2	75.5
Ssc.21934.1.A1_at, CF794827	393.5	402.6	347.2	447.2	612.8	239.9	313.4	395.7	125.7	373.4
Ssc.8567.1.A1_at, BF711960, RPL35A	272.3	220.9	185.6	259.6	153.8	344.6	287.0	344.6	472.4	323.0
Ssc.15552.1.S1_at, BP162471, BOP1	401.1	573.5	261.6	389.0	931.2	174.0	195.0	286.0	92.9	213.3
Ssc.24386.1.S1_a_at, CF362365, TRIP6	602.7	632.6	653.9	518.5	511.1	776.9	896.5	963.8	931.3	859.5
Ssc.8321.1.A1_at, BF712745, GPC5	234.1	208.3	189.8	292.4	228.0	81.7	114.1	215.9	206.0	109.3
Ssc.10820.1.A1_at, CO942708, C18orf8	71.4	86.2	84.4	133.1	158.8	30.5	63.1	66.6	36.9	74.5
Ssc.21331.1.A1_at, BI401770	373.5	349.4	496.5	325.3	338.8	572.0	489.4	677.5	534.4	581.8
Ssc.18799.1.S1_at, BX670013, DAB2IP	1119.7	852.5	1372.4	799.9	629.8	1715.7	1361.4	836.7	1894.7	1379.9
Ssc.4626.3.S1_at, CN156700, IPO4	98.4	97.8	89.3	123.6	101.7	114.3	155.2	129.9	241.2	134.5
Ssc.12131.1.A1_at, BI401049, TGFB2	745.7	641.0	520.6	981.4	423.4	335.5	399.1	468.2	351.1	528.2
Ssc.27622.1.S1_at, BG894437, KLF11	488.3	537.8	241.4	182.8	183.7	661.7	544.3	335.0	488.0	561.3
Ssc.21036.1.S1_at, CK460060, CDK5R1	268.8	173.7	200.7	257.8	259.8	59.2	94.2	215.3	141.1	131.1
Ssc.24891.1.S1_at, CK465770, TRIM22	674.7	770.9	391.8	1125.6	1269.4	214.1	348.4	751.9	289.6	522.4
Ssc.10489.1.A1_at, BF702274, CDC27	132.4	210.8	139.6	115.7	129.8	321.5	287.3	140.5	246.5	271.0
Ssc.18715.1.A1_at, BX914874, CITED4	384.2	505.6	751.2	628.6	522.6	186.3	213.7	503.4	146.1	523.0
Ssc.1075.1.A1_at, BF712416, C10orf65	285.8	372.0	264.0	562.5	624.3	263.0	283.6	326.5	156.0	311.5
Ssc.15822.1.S1_at, NM_214120.1, F5	527.0	120.9	221.9	110.4	85.1	108.9	140.6	133.2	127.5	157.4
Ssc.15103.2.S1_at, CN162154, HYAL3	694.4	547.5	824.1	278.4	392.0	1169.0	1174.6	776.9	1403.6	794.2
Ssc.5372.1.S1_at, BX666499, NFRKB	556.5	393.8	450.3	456.8	440.1	233.3	207.1	240.3	66.2	358.8

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
30.9	76.8	68.7	16.1	18.3	41.3	62.8	108.7	42.0	32.2	54.4	25.6	0.668842195	0.386680164
1776.0	1831.9	1885.8	1478.1	1309.5	5014.0	2951.5	5734.0	2215.9	939.6	1060.6	1388.9	0.750754973	0.386449039
71.7	82.5	46.6	64.1	51.5	50.7	323.4	158.6	61.2	77.5	38.3	14.1	0.189199497	0.385722692
1319.9	832.6	1058.9	734.6	544.1	911.9	1436.2	2334.8	900.3	464.3	467.6	268.4	0.626868304	0.385621363
366.3	372.2	253.0	318.9	192.3	475.1	1622.1	854.9	329.6	332.3	244.9	99.2	0.203218952	0.385599201
359.1	68.2	154.7	382.4	134.1	92.0	1204.0	515.5	198.4	557.0	168.9	137.1	0.164797896	0.384886458
28.5	16.1	10.9	29.4	15.4	7.5	109.2	46.7	18.0	56.4	23.0	9.1	0.164590204	0.384560502
612.1	627.2	523.5	343.9	498.1	478.6	611.4	1336.4	513.9	131.2	584.8	102.9	0.840584925	0.384540557
152.1	52.2	107.9	63.4	44.1	107.1	131.2	228.8	87.8	31.7	81.0	41.7	0.669105319	0.383741259
530.8	343.8	521.0	333.4	704.4	317.1	1886.8	1196.4	458.4	307.7	417.3	153.9	0.242962437	0.383156974
384.8	172.3	352.7	141.6	334.2	324.3	486.2	743.8	285.0	144.1	165.3	101.8	0.586192474	0.383145111
852.8	146.3	496.2	149.8	424.9	671.4	489.6	1193.2	456.9	174.3	641.9	281.5	0.933172665	0.382932716
144.9	192.0	111.2	145.7	130.0	114.9	674.2	365.6	139.8	160.9	57.6	29.4	0.207344448	0.382318619
696.7	927.2	587.0	304.8	343.8	1661.4	3532.2	1977.6	753.5	994.6	475.3	500.9	0.213320839	0.381001261
187.7	121.7	99.2	104.4	64.0	124.9	743.8	307.5	117.0	208.5	135.6	40.9	0.157277942	0.380433604
241.0	103.9	124.7	150.3	119.9	193.0	227.4	408.7	155.5	56.7	163.8	52.2	0.683610354	0.380393116
717.1	331.4	564.2	228.9	307.5	758.4	835.5	1276.3	484.6	364.7	482.0	226.1	0.580005905	0.379666338
1661.8	814.2	1216.2	663.3	845.1	1523.9	1626.2	2952.2	1120.8	454.4	1240.4	410.8	0.689174896	0.379629567
453.9	445.5	393.3	386.7	383.6	337.0	1806.3	1053.8	400.0	447.5	433.9	43.4	0.221447157	0.379593076
44.3	94.2	38.9	62.5	41.2	51.4	240.8	146.1	55.4	64.0	58.0	20.8	0.230173894	0.379306411
47.5	50.4	21.1	42.1	27.4	32.0	164.9	96.9	36.8	43.5	20.8	11.7	0.222916414	0.379100475
4171.6	2311.3	2682.7	2172.4	2711.8	2718.4	4792.4	7379.4	2794.7	639.8	629.7	713.0	0.583147624	0.378714374
171.9	161.0	171.1	100.5	107.3	180.0	254.2	393.2	148.6	65.3	95.5	35.2	0.584618209	0.378009495
337.6	349.3	416.6	370.8	68.5	159.8	1442.0	751.0	283.8	742.8	562.2	137.2	0.196792329	0.377841691
253.8	262.1	147.8	131.3	161.1	235.9	349.9	526.7	198.7	83.9	130.1	58.3	0.567748819	0.377162674
505.1	155.1	540.2	262.2	418.3	502.6	557.0	1055.7	397.3	130.9	424.1	155.2	0.713170084	0.376290613
210.8	103.4	235.7	146.6	159.0	47.1	1144.6	400.8	150.4	580.7	384.3	69.1	0.131428738	0.375295213
664.0	367.7	584.0	278.4	425.7	483.2	580.7	1249.2	467.2	208.7	450.7	141.3	0.804516544	0.373972676
306.3	326.7	227.8	296.7	166.2	219.2	1095.7	687.7	257.2	250.4	102.5	62.3	0.23469872	0.373949335
90.0	91.2	142.3	60.2	109.5	114.0	157.2	270.9	101.2	21.3	126.4	27.7	0.64368401	0.373542005
162.4	202.3	150.1	173.8	155.8	146.9	675.0	443.2	165.2	209.0	86.2	20.5	0.24475818	0.372798111
178.4	296.4	163.1	209.8	114.0	168.3	1070.5	505.3	188.3	352.9	126.8	61.3	0.175926964	0.372745385
71.9	72.6	77.2	80.9	79.7	58.9	323.0	198.0	73.5	57.5	35.9	8.0	0.227671476	0.371455513
17.8	57.4	57.2	30.3	39.0	37.5	71.0	107.5	39.9	21.3	23.6	15.4	0.561502347	0.37078373
56.5	26.6	34.8	13.5	22.0	59.0	60.5	95.5	35.4	20.3	47.0	18.7	0.585511082	0.370603015
1293.7	715.4	928.9	518.1	684.1	818.4	1395.5	2240.3	826.4	453.2	392.1	267.0	0.592196091	0.368887461
59.4	66.6	38.7	82.4	53.5	58.8	354.3	162.5	59.9	96.9	72.1	14.4	0.169065763	0.368570022
151.0	152.9	237.0	99.4	140.0	204.5	256.0	445.4	164.1	79.2	248.8	49.0	0.641195927	0.368474617
43.4	69.5	41.1	55.9	81.8	15.6	245.1	139.0	51.2	82.3	59.8	23.3	0.208962328	0.368465228
559.3	203.3	295.5	348.4	214.5	469.5	624.2	946.1	348.4	220.6	388.8	142.1	0.558199024	0.368281786
485.1	286.2	348.2	207.9	176.8	554.4	620.9	932.1	343.1	217.1	206.8	151.0	0.552584957	0.368085654
2.0	32.2	30.9	23.0	19.6	23.0	128.1	59.2	21.8	41.3	15.6	10.9	0.170075994	0.367837442
144.6	128.6	65.0	111.2	98.7	90.0	440.7	289.6	106.4	102.6	109.7	28.3	0.241342532	0.367205304
104.3	98.8	187.2	121.2	151.5	115.9	218.4	354.3	129.8	49.6	70.1	33.6	0.594289813	0.366382554
103.8	71.7	63.5	95.3	27.1	60.8	511.3	192.2	70.4	259.6	69.7	27.4	0.137628436	0.366035511
282.2	358.3	309.2	322.3	422.3	249.9	583.8	885.6	324.0	65.6	72.1	60.5	0.555079713	0.365891298
67.3	68.3	61.0	49.8	41.3	31.5	230.5	145.4	53.2	38.7	61.2	14.9	0.230782579	0.365887208
6.7	11.2	17.9	38.1	12.9	32.4	106.8	54.3	19.9	37.3	19.4	12.6	0.186052319	0.365733922
167.9	234.8	208.4	197.6	260.4	183.4	376.7	571.0	208.8	69.3	69.7	34.0	0.5541545	0.365573885
804.8	519.0	556.5	306.9	442.3	521.7	954.9	1437.7	525.2	292.3	405.1	163.5	0.550028276	0.365310778
47.4	59.3	78.1	35.9	60.9	58.1	102.2	155.0	56.6	12.8	50.3	14.2	0.554196032	0.365221692
190.6	272.0	181.3	72.9	129.3	66.1	662.4	416.4	152.0	215.9	81.1	78.6	0.229511991	0.365096137
264.7	185.1	176.2	233.5	161.5	110.8	326.8	518.1	188.6	172.6	120.0	54.3	0.577213382	0.364114839
45.3	57.5	67.1	53.7	31.0	25.3	232.2	128.2	46.7	42.3	58.5	16.1	0.200939008	0.363941333
116.1	241.1	179.6	243.4	74.5	73.2	846.5	425.3	154.7	353.1	215.1	78.1	0.18269776	0.363642777
69.7	59.6	79.2	61.5	115.4	165.9	145.7	253.4	91.9	37.4	68.7	41.6	0.630806902	0.362659194
171.2	69.6	114.0	110.9	120.7	97.0	558.4	314.5	113.9	138.3	183.1	33.4	0.203961034	0.362162162
70.9	150.6	102.8	83.3	88.6	86.2	421.7	268.1	97.1	163.3	67.3	28.2	0.230168516	0.362026953
82.8	48.0	32.8	29.6	64.9	31.9	213.1	133.5	48.3	183.1	17.8	21.6	0.226853156	0.36199321
485.7	327.7	366.6	274.8	270.8	575.7	547.3	1063.7	383.6	220.6	271.0	122.7	0.700829557	0.360594551
79.3	67.3	86.7	107.6	70.9	65.7	459.5	221.1	79.6	59.6	104.5	15.8	0.173195502	0.359877604

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.4756.1.A1_at, CF175894, ADORA3	162.4	148.9	151.6	314.4	491.9	161.8	127.7	272.4	135.0	127.2
Ssc.11365.1.A1_at, BQ604982	65.1	70.4	98.4	113.0	89.2	32.0	42.1	75.8	18.2	73.8
Ssc.28499.1.S1_at, CK465623, FAM60A	81.7	48.3	83.0	72.9	118.5	115.8	196.5	104.4	204.1	114.4
Ssc.5086.2.S1_at, AW478197, POLR2C	480.2	379.0	482.0	177.2	234.9	668.0	532.0	296.3	758.4	573.3
Ssc.23921.1.S1_at, BF080228, RNGTT	1017.1	898.5	1107.9	1216.8	1220.4	368.1	502.7	761.3	325.7	661.9
Ssc.8441.1.A1_at, BQ600297	1324.8	1254.7	1235.6	1567.2	1351.9	740.0	705.9	929.4	710.3	1280.4
Ssc.11109.1.S1_at, NM_213939.1, PIK3CG	402.9	479.5	226.9	718.3	721.9	214.8	347.1	449.4	147.4	176.8
Ssc.17133.1.A1_at, BI400897, IDH2	575.4	552.4	910.1	236.5	350.0	1611.8	2412.9	920.1	2294.3	756.9
Ssc.24969.1.S1_at, CK465631, KRCC1	470.0	599.4	358.6	657.9	760.2	392.4	246.3	249.1	108.0	411.6
Ssc.8601.1.A1_at, BF712886, DPYD	491.1	580.6	450.2	1039.3	708.2	307.4	246.6	429.2	131.6	372.3
Ssc.19382.1.A1_at, CF180618, PCK2	82.4	64.3	75.7	50.5	62.1	94.3	147.3	88.6	144.7	82.0
Ssc.3872.1.S1_at, BQ604389, FLT1	354.1	273.2	392.5	43.9	246.9	604.6	643.6	120.1	428.4	230.3
Ssc.3517.2.S1_at, BX667243, CTSA	630.1	477.3	638.2	617.2	709.0	348.0	313.5	417.0	455.3	495.1
Ssc.16640.2.S1_at, CB479843, VSIG4	68.5	54.5	80.2	66.9	116.1	41.5	47.7	86.0	24.5	35.4
Ssc.29723.1.A1_at, CO944594, ACTR3B	749.6	1102.5	806.0	614.4	756.2	316.6	766.5	565.3	254.1	352.0
Ssc.9991.1.S1_at, NM_213916.1, PTHLH	2724.8	3357.0	3701.3	1579.2	1851.5	8401.4	3540.2	1847.7	7698.4	3108.3
Ssc.7839.1.A1_at, BQ599567, EPB41L3	486.1	473.6	333.9	2172.3	1143.5	338.4	220.3	601.3	163.3	231.7
Ssc.10760.1.A1_at, BQ597904, THNSL1	91.1	102.2	60.1	124.0	96.9	97.6	51.5	71.8	22.0	73.3
Ssc.20706.1.S1_at, BX676130, HOXB6	949.5	1015.1	777.6	1191.2	1080.5	407.6	624.6	900.7	615.2	684.2
Ssc.15583.1.S1_at, CF175347, GHR	161.1	125.2	97.7	279.1	228.4	229.4	224.3	295.7	318.7	414.7
Ssc.10655.1.S1_at, BX671606, ZNF33B	164.3	148.1	100.6	142.9	155.2	73.0	111.2	71.7	93.0	75.4
Ssc.11348.1.A2_at, CB480026, CCT6A	2665.1	2968.9	3313.9	2824.4	2048.9	4724.1	4014.0	4179.8	4452.6	3724.2
Ssc.24728.2.S1_at, CK466412, UCK2	601.7	483.8	678.3	210.5	246.8	963.9	1365.7	491.5	1714.0	624.5
Ssc.14047.2.A1_at, BI399028, KIAA1217	108.9	184.7	243.5	195.6	302.8	94.0	86.7	158.7	66.6	209.7
Ssc.9598.1.A1_at, BF711007, PGM5	339.9	235.9	253.6	431.6	258.7	109.1	164.5	212.7	117.2	210.6
Ssc.15237.1.S1_at, NM_001001630.1, PDZD11	367.0	403.9	380.4	510.2	591.6	370.0	238.3	305.1	171.2	411.0
Ssc.10388.2.S1_at, CK457975, PPAN	1131.2	1084.3	1155.0	673.4	755.2	1461.6	1789.4	1370.3	2640.2	1296.5
Ssc.29562.1.A1_at, CO941969	562.4	629.4	582.9	975.7	722.4	425.1	328.7	605.4	253.5	535.1
Ssc.5735.1.A1_at, CK450823, NT5DC2	1139.8	1302.9	731.4	1412.6	2045.2	486.1	490.0	1315.2	480.2	560.8
Ssc.24283.1.S1_at, CK465898, RNMTL1	392.0	401.4	401.4	245.2	229.8	399.7	573.5	485.5	804.3	403.6
Ssc.2472.1.S1_at, CN160167, CYB5D2	201.8	177.5	153.1	185.4	254.2	131.6	64.4	136.3	77.9	84.1
Ssc.4899.1.S1_at, BF711239, SRPX2	295.9	213.4	318.2	219.5	178.7	248.9	429.1	501.5	476.0	282.6
Ssc.27592.1.S1_at, CK458742, CH25H	467.4	411.0	400.4	911.0	879.2	183.5	263.9	406.0	156.9	449.0
Ssc.27272.1.A1_at, CK454749, PROC	335.0	343.4	209.9	130.2	359.2	214.2	144.4	213.0	148.8	164.0
Ssc.17159.1.S1_at, CK461355	2226.2	2621.5	1903.3	2813.6	4522.2	1837.0	852.9	3050.6	1872.3	1691.9
Ssc.6425.1.A1_at, CF176014, ABCC5	280.0	150.7	189.9	344.4	300.2	133.8	118.8	298.6	120.6	90.4
Ssc.11966.1.S1_at, CD572704, SHMT2	782.5	780.7	1011.6	685.3	679.7	1232.9	1355.0	1071.6	1447.9	990.6
Ssc.29187.1.A1_at, CO951491, GJA1	918.0	1586.7	1119.0	188.1	1106.6	1438.7	2268.0	391.4	2775.6	996.4
Ssc.5627.1.S1_at, CO943392, NOL5A	3176.2	2688.5	3283.6	1906.0	2120.8	3350.0	3881.0	3957.9	6153.2	3208.4
Ssc.9681.1.A1_at, BF711226, YWHAZ	58.4	65.3	41.1	31.8	25.2	92.0	63.7	56.6	108.0	55.6
Ssc.25289.1.S1_at, BP436550, CDK6	262.6	353.2	348.8	35.3	232.1	446.7	665.9	157.6	557.3	386.0
Ssc.31130.1.A1_at, CN153555, IGF1	663.6	1752.4	525.5	1532.7	1423.0	470.2	147.3	361.2	98.3	964.2
Ssc.4492.1.A1_at, CN154066, C6orf103	358.6	322.2	265.2	464.0	456.0	269.4	231.5	204.9	96.2	404.7
Ssc.7376.1.A1_at, BI182523, EDEM2	1156.0	1148.1	949.6	1439.4	1577.4	735.7	650.0	1024.7	523.9	1177.0
Ssc.25276.1.S1_at, CK462934, LASS2	305.8	454.3	530.6	94.2	283.3	589.3	676.0	224.0	713.0	439.7
Ssc.21197.1.A1_at, CB468961, ABCF2	1430.9	1343.7	1681.9	891.1	903.9	1782.6	2167.7	1451.8	2623.2	1470.7
Ssc.18184.1.S1_at, CF176363, ZC3H13	1381.0	1545.7	1198.9	1495.4	1738.8	690.9	800.9	693.0	332.0	712.4
Ssc.12578.1.A1_at, BI402878, IGF1	996.9	2300.2	798.0	1818.1	1982.3	716.5	171.3	622.5	136.5	1386.6
Ssc.14415.1.A1_at, BQ602223, DTX3L	797.4	1136.3	972.6	1561.3	1120.7	510.4	624.6	835.7	452.0	902.5
Ssc.20783.1.S1_at, CN159200, ANKRD52	1531.3	1251.4	1460.6	490.1	895.7	1341.3	2319.4	1880.0	3214.0	998.1
Ssc.5624.1.A1_at, BQ603307, NEK4	382.4	344.5	295.3	327.9	136.2	136.5	316.0	200.9	143.5	152.5
Ssc.21541.1.S1_at, CF793050, ACAD10	263.5	249.3	207.4	241.9	253.0	168.7	153.3	139.2	125.4	212.5
Ssc.20030.1.S1_at, AW359795, ZMIZ1	806.2	825.4	974.2	363.3	437.3	1490.4	818.9	695.7	1462.9	812.7
Ssc.18091.1.A1_at, CF179812	274.6	323.6	125.9	395.0	571.5	198.2	172.2	205.8	144.4	320.0
Ssc.5642.1.S1_at, CK453723, PARP4	40.3	84.6	46.0	117.5	64.9	41.6	30.5	42.3	24.8	35.0
Ssc.19076.1.S1_at, CF367547, KIF16B	127.8	147.7	68.9	88.3	166.1	42.6	94.6	71.1	24.6	56.9
Ssc.25047.1.A1_at, CK451219, LYPLAL1	928.9	997.8	796.9	482.2	555.3	844.6	1154.5	785.9	1927.3	939.3
Ssc.8555.1.A1_at, CO947267, IDH2	1922.2	1602.3	4040.4	1746.7	895.7	5545.8	5843.0	4879.8	5516.8	2115.3
Ssc.10326.1.A1_at, BI400600, STK39	286.1	243.0	211.9	321.0	271.3	84.1	139.4	151.9	83.6	209.4
Ssc.2238.1.S1_at, BE033096, INTS3	328.4	285.7	387.3	471.4	473.2	269.5	250.4	349.8	89.9	300.7
Ssc.11902.1.A1_s_at, BI185754, TADA3L	399.7	283.1	332.3	542.5	516.2	360.7	207.8	331.2	133.9	342.2

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
119.3	16.9	40.5	96.6	42.5	39.6	253.8	164.8	59.2	150.1	61.8	39.5	0.233349091	0.359381952
15.3	30.5	9.9	16.1	7.8	24.7	87.2	48.4	17.4	19.8	25.6	8.7	0.199304441	0.359308254
43.4	58.6	83.4	38.3	54.1	39.1	80.9	147.0	52.8	25.2	48.9	17.1	0.653025058	0.359199311
292.7	142.6	290.1	126.5	108.4	252.4	350.7	565.6	202.1	139.9	174.2	85.5	0.576389285	0.357349128
267.1	169.5	195.2	208.6	161.1	121.0	1092.1	523.9	187.1	137.3	186.7	49.6	0.171299772	0.357070148
361.7	314.0	299.1	316.3	233.4	343.4	1346.8	873.2	311.3	132.2	245.6	44.3	0.231145991	0.356523897
125.4	43.2	72.5	173.0	71.9	85.3	509.9	267.1	95.2	212.6	127.3	46.5	0.186735961	0.356483215
655.0	275.0	836.1	58.6	502.8	1086.4	524.9	1599.2	569.0	257.6	760.9	373.6	1.084025555	0.35579248
77.0	163.0	70.7	138.4	81.2	69.8	569.2	281.5	100.0	157.7	124.1	40.2	0.175708279	0.355324239
102.3	149.1	70.1	119.7	66.6	125.7	653.9	297.4	105.6	237.1	115.3	32.5	0.161472034	0.354997422
48.5	41.0	31.1	32.8	29.6	54.2	67.0	111.4	39.5	12.4	31.9	10.1	0.590049751	0.354941043
221.8	93.0	194.8	66.2	40.4	245.5	262.1	405.4	143.6	135.5	228.6	87.5	0.547904268	0.354259168
137.3	208.9	149.7	129.6	70.5	166.4	614.4	405.8	143.7	84.5	74.9	45.6	0.233956204	0.354214928
26.3	10.4	10.6	15.1	20.1	17.3	77.2	47.0	16.6	23.6	23.4	6.1	0.215346107	0.353750177
35.4	211.1	255.8	119.9	31.3	299.9	805.7	450.9	158.9	180.5	211.7	114.1	0.197210018	0.352406299
1271.1	1381.4	1477.6	607.9	615.6	5005.2	2642.8	4919.2	1726.5	921.2	2935.3	1650.7	0.65328167	0.350964927
206.8	20.3	64.9	234.0	74.2	51.5	921.9	311.0	108.6	766.4	174.2	88.9	0.11782083	0.349249732
21.3	39.2	15.8	15.9	12.3	27.7	94.9	63.2	22.0	23.1	28.3	10.0	0.23227212	0.34840818
196.7	363.5	275.3	212.0	151.0	152.5	1002.8	646.5	225.2	154.3	176.5	81.7	0.224542439	0.348307191
103.7	122.1	85.7	102.6	65.9	139.2	178.3	296.6	103.2	74.6	77.7	25.9	0.578799776	0.347990289
28.2	32.9	26.3	34.7	33.3	21.7	142.2	84.9	29.5	24.6	17.1	5.0	0.207542305	0.347827795
1752.6	1482.0	1994.2	853.2	1049.2	1670.1	2764.2	4218.9	1466.9	466.1	386.7	436.4	0.530664245	0.34769002
472.4	255.4	444.3	124.6	233.8	619.9	444.2	1031.9	358.4	209.0	509.7	184.1	0.806807438	0.347313745
35.1	56.3	28.3	48.8	41.7	45.7	207.1	123.1	42.7	72.0	59.4	10.0	0.20593916	0.346353744
34.8	104.8	42.3	85.1	40.4	29.8	303.9	162.8	56.2	81.9	49.3	31.0	0.184904915	0.345166441
84.0	97.2	92.7	108.3	59.5	176.6	450.6	299.1	103.1	96.9	97.0	39.6	0.228684923	0.344510564
582.1	581.8	623.5	391.9	462.4	896.0	959.8	1711.6	589.6	227.4	552.2	173.4	0.614299209	0.344482745
159.4	218.7	138.4	129.2	91.0	148.1	694.6	429.6	147.5	168.8	144.3	42.0	0.212316671	0.343297017
225.8	317.1	200.4	348.2	132.5	145.0	1326.4	666.5	228.2	477.9	364.1	88.5	0.172022095	0.34235613
285.8	177.6	173.9	104.7	131.4	215.3	334.0	533.3	181.5	88.3	167.3	64.0	0.543328542	0.340227256
26.4	43.0	25.5	45.7	14.2	46.8	194.4	98.9	33.6	37.8	32.9	13.4	0.172839506	0.33987457
152.8	94.1	168.4	74.1	109.6	190.9	245.1	387.6	131.7	59.1	114.9	45.9	0.537040059	0.339636758
83.7	104.8	88.7	172.8	57.3	87.2	613.8	291.9	99.1	258.3	130.8	39.2	0.161426089	0.339489253
54.7	51.4	69.8	89.7	50.7	41.7	275.5	176.9	59.7	100.7	34.3	17.3	0.216544482	0.337328509
1004.4	199.0	364.6	1173.1	451.3	572.5	2817.4	1860.9	627.5	1016.1	784.3	381.2	0.222720324	0.337186225
48.9	52.7	50.4	49.1	63.7	42.8	253.0	152.4	51.3	80.2	83.2	6.9	0.202603014	0.336307181
458.4	394.5	443.3	266.2	406.7	486.4	788.0	1219.6	409.3	134.5	190.4	77.7	0.519379156	0.33556084
849.0	369.4	508.1	188.6	294.4	953.3	983.7	1574.0	527.1	508.5	958.6	309.6	0.535878877	0.334896211
1890.4	956.4	1622.7	770.1	988.7	2028.0	2635.0	4110.1	1376.1	614.9	1187.5	537.4	0.52221615	0.334797207
20.2	26.7	20.8	26.8	25.3	30.9	44.4	75.2	25.1	17.1	23.6	4.0	0.566200781	0.33408708
223.2	109.4	122.2	90.8	100.3	240.8	246.4	442.7	147.8	129.3	192.0	66.3	0.599770022	0.333822754
222.2	123.2	99.9	192.1	106.6	72.9	1179.4	408.2	136.2	549.1	346.2	58.1	0.115436139	0.333504801
71.8	121.5	65.2	87.9	63.0	72.3	373.2	241.3	80.3	86.0	111.8	22.0	0.215121472	0.332656556
268.7	358.0	238.6	355.4	153.9	264.3	1254.1	822.3	273.2	251.2	270.7	76.8	0.217805598	0.332194196
250.3	141.5	162.8	139.3	120.4	238.8	333.6	528.4	175.5	168.8	200.1	55.3	0.526066019	0.332166288
900.6	587.1	760.4	417.0	411.6	707.5	1250.3	1899.2	630.7	345.2	498.4	195.5	0.504438935	0.332087195
202.8	279.3	208.6	298.9	98.8	198.1	1472.0	645.8	214.4	200.0	181.1	70.9	0.145667455	0.331996573
327.9	175.3	162.0	280.0	152.4	110.7	1579.1	606.7	201.4	649.8	507.7	83.7	0.12753045	0.331943254
134.5	254.7	187.3	269.8	86.9	386.0	1117.7	665.0	219.9	283.2	197.8	107.1	0.196720529	0.33060668
664.6	564.9	851.0	426.2	656.5	692.1	1125.8	1950.6	642.6	432.8	868.3	141.0	0.57073955	0.329418218
44.6	66.8	44.6	85.4	63.0	70.6	297.3	189.9	62.5	95.3	74.9	15.8	0.21025365	0.329155256
52.6	50.6	46.4	65.7	50.7	49.2	243.0	159.8	52.5	21.4	33.6	6.8	0.216168765	0.328703124
461.8	292.9	494.4	177.0	327.1	329.2	681.3	1056.1	347.1	265.9	387.1	116.1	0.509433224	0.328624272
83.6	81.7	71.8	78.6	43.4	51.2	338.1	208.1	68.4	163.5	67.0	17.0	0.202245751	0.328576462
7.4	8.1	13.7	9.2	18.6	11.5	70.7	34.8	11.4	31.4	7.4	4.2	0.161571846	0.327688481
17.3	22.5	20.6	21.9	16.4	15.1	119.8	58.0	19.0	40.5	26.8	3.1	0.1583723	0.327237175
430.3	438.1	355.1	301.0	311.6	376.9	752.2	1130.3	368.8	226.5	467.0	57.8	0.490326412	0.326308774
1336.0	777.8	2054.5	164.5	1495.2	3515.2	2041.5	4780.1	1557.2	1183.5	1530.5	1155.9	0.762787417	0.325764517
46.7	54.8	28.5	83.8	22.6	24.7	266.7	133.7	43.5	41.6	52.6	23.6	0.16319158	0.325528626
68.8	71.8	75.5	80.5	75.9	119.5	389.2	252.1	82.0	84.0	98.1	18.8	0.210688592	0.325319368
81.5	87.0	74.3	109.3	69.7	113.6	414.8	275.2	89.2	112.9	99.3	18.3	0.215144501	0.324296167

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.24083.1.A1_at, CK455873	294.5	217.3	289.3	231.9	324.7	187.2	237.1	107.9	96.5	147.1
Ssc.6454.1.S1_at, BQ602900	85.8	175.6	121.7	166.1	267.7	131.8	132.3	81.7	44.5	139.8
Ssc.25641.1.S1_at, AJ660139, CDK6	99.8	67.0	96.6	79.7	43.9	96.5	139.9	102.4	210.9	112.0
Ssc.12416.3.A1_at, CN160520, FNBP4	46.7	61.8	22.6	27.6	55.7	130.0	73.3	45.9	90.9	28.3
Ssc.30823.1.S1_at, BP436131, ABI3BP	2752.7	2483.2	3044.4	1703.9	1792.3	3885.8	3862.9	2259.6	5339.9	3109.9
Ssc.151.1.S1_at, NM_214043.1, CYBB	590.4	421.8	376.7	781.8	1130.2	209.5	162.0	526.1	212.4	261.1
Ssc.14532.1.S2_at, CN166686, FUT8	2512.8	2334.2	2387.3	5186.0	4492.9	1521.8	1837.0	3039.1	1162.4	2877.3
Ssc.28155.1.A1_at, CN029252, C3orf26	505.2	584.4	706.3	326.0	347.2	455.4	1100.0	965.0	962.4	762.9
Ssc.19231.2.S1_at, BG383566, FARSA	268.1	255.1	311.5	93.2	194.5	422.7	453.1	185.3	468.9	323.0
Ssc.21998.2.S1_at, BX674936, MCF2L	135.4	139.9	116.5	172.1	336.6	112.9	60.8	138.5	127.8	93.9
Ssc.11839.1.S1_at, CF790572, ZNF462	911.6	760.0	476.0	728.7	847.0	139.9	264.8	400.2	359.0	486.0
Ssc.3041.1.S1_at, BI404922, FAM161A	186.0	153.5	109.7	206.5	191.4	73.2	77.6	106.6	69.7	83.9
Ssc.4645.1.A1_at, BQ599647	650.0	739.5	554.5	1234.4	969.8	522.4	436.1	490.2	209.7	657.4
Ssc.3548.1.S1_at, BX914784, CDKAL1	932.9	472.6	1353.7	630.7	704.1	1469.9	1393.2	1495.5	1235.6	1099.2
Ssc.9170.1.A1_at, CN166727, PRKD1	705.5	838.5	553.6	1387.6	1078.2	376.3	366.5	635.9	230.3	692.4
Ssc.27140.1.A1_at, CN167133, PTPN2	178.0	152.7	134.4	115.9	209.3	96.4	82.5	81.1	99.8	79.1
Ssc.14297.1.S1_at, CK456073, CHURC1	476.7	718.7	524.7	756.9	802.1	498.9	353.7	483.7	232.4	454.8
Ssc.13587.1.A1_at, CF792676, ANK3	4078.4	3515.3	2649.6	4427.1	3579.8	1608.1	1205.3	1705.9	960.2	1734.6
Ssc.2163.2.A1_at, CO947282, CIRBP	666.4	422.5	355.9	478.1	653.5	262.0	262.4	341.6	288.9	325.6
Ssc.11487.1.A1_at, BI181266, PRR15	1314.9	705.0	326.6	1234.9	703.3	338.1	264.3	398.1	168.9	677.4
Ssc.10968.1.S1_at, CN163084	3763.8	4051.9	3107.2	6319.6	5524.1	2683.2	2525.8	4003.5	2383.1	2845.3
Ssc.7283.1.A1_at, BQ598473, SOX5	62.5	44.8	60.1	145.5	97.0	32.2	30.8	66.3	79.3	47.4
Ssc.25850.1.A1_at, BM659769, PTGES3	1190.4	1232.1	1668.9	327.5	1049.5	1479.4	1658.8	1236.5	2387.2	1485.0
Ssc.29833.1.A1_at, CO937108, AHCTF1P	323.0	94.7	199.6	92.2	65.2	289.6	171.1	140.2	678.3	73.1
Ssc.20177.1.S1_at, NM_001001865.1, SPI1	178.5	133.6	108.1	262.5	320.6	90.7	72.5	135.6	133.1	88.2
Ssc.11439.1.A1_at, BI182561	281.0	241.7	521.6	214.7	230.4	551.7	596.8	646.2	415.4	240.5
Ssc.30189.1.A1_at, CO987781, MYCBP2	335.1	464.6	117.4	252.1	452.8	172.1	110.2	93.5	147.0	232.3
Ssc.19959.1.S1_at, CN163183, KIAA1324L	505.4	320.3	353.3	403.5	218.9	367.0	642.9	501.0	926.8	458.7
Ssc.26492.1.A1_at, CN070048, KLF11	180.9	261.5	136.9	153.7	117.4	364.6	272.3	277.6	314.4	375.6
Ssc.23854.1.S1_at, CN153466, EEA1	181.9	152.9	190.1	67.5	116.9	192.9	266.1	184.2	298.4	144.5
Ssc.27135.1.A1_at, CN167099, FOXS1	1186.8	1438.7	1318.2	423.3	481.2	3008.4	753.4	711.9	2108.6	1183.7
Ssc.14320.1.A1_at, BQ601835, TDRD3	245.1	477.6	306.1	348.0	424.3	162.5	155.9	171.0	103.3	246.5
Ssc.10950.1.A1_at, CF359715, C10orf104	969.7	895.3	735.0	989.1	855.4	800.5	323.2	531.4	249.2	680.0
Ssc.6272.1.A1_at, BQ598778, SYNCRIP	640.7	819.7	681.9	252.1	524.1	1068.6	1294.4	338.2	1456.6	755.3
Ssc.17942.1.A1_at, CF176409, ELOVL7	104.8	71.0	119.4	150.3	102.6	78.5	93.2	82.1	33.5	53.2
Ssc.4394.1.S1_at, CK455674, SUV420H1	569.8	546.6	554.1	583.2	592.1	386.5	332.2	398.3	182.9	408.3
Ssc.20236.1.A1_at, CO941195, LRRN2	244.9	279.9	161.2	261.1	253.6	140.1	141.9	185.7	180.8	106.6
Ssc.3237.1.S1_at, CN158098	769.8	662.4	967.4	469.6	532.2	892.4	1147.8	862.9	1539.9	835.8
Ssc.21018.1.S1_at, CN158985, SUV420H1	813.8	899.3	823.4	1236.3	788.5	613.8	608.2	610.7	556.9	588.6
Ssc.1176.1.A1_at, BM190033, TGFBR3	449.2	521.8	416.8	937.0	802.5	160.9	330.2	278.7	112.8	342.1
Ssc.24960.1.S1_at, CK464888, OR52I2	126.1	136.4	75.3	205.5	213.4	88.5	118.2	88.4	67.5	106.5
Ssc.27521.1.S1_at, CO949260, ABCD4	653.8	636.8	711.3	608.2	1287.6	317.8	562.0	495.8	296.3	716.3
Ssc.3107.2.A1_at, CF368812, CLEC14A	5559.8	7425.4	5781.8	8080.5	8644.9	3876.3	4499.8	4832.4	3738.4	6075.4
Ssc.22376.1.A1_at, CF792416, TSR1	2001.3	2127.1	2381.5	1329.9	1470.0	2052.9	2757.7	2667.2	4814.6	2382.4
Ssc.6154.2.S1_at, CF368283	839.5	750.6	819.8	499.3	587.8	1193.4	876.3	816.4	1576.1	942.3
Ssc.16640.1.A1_at, CF368312, VSIG4	619.1	486.3	406.1	1447.0	1645.8	256.5	158.7	383.5	116.5	238.2
Ssc.22092.1.S1_at, CF365067, GPC6	422.2	521.0	526.6	889.5	480.8	367.0	311.5	445.0	210.5	418.1
Ssc.31065.1.A1_at, CO942840	250.1	305.5	306.7	259.8	199.6	305.4	390.9	492.3	406.1	493.0
Ssc.21959.1.S1_at, CN158067, CARS	1852.7	1792.4	1946.0	1056.4	1350.8	2102.5	2787.0	2032.9	3569.1	1735.2
Ssc.6182.1.A1_at, BQ599935, RANBP1	149.2	99.4	165.7	56.7	84.1	136.9	170.9	111.2	244.6	174.2
Ssc.19011.1.S1_at, CF787184, SLC7A6OS	242.0	178.2	264.5	110.1	230.2	321.3	431.8	275.5	653.9	191.6
Ssc.16687.1.S1_at, CN158140, YARS	1905.9	1173.6	2040.7	780.3	923.8	1913.7	2548.1	1910.1	2928.2	1999.0
Ssc.44.1.S1_at, NM_214002.1, ITGB3	483.1	371.9	601.7	358.7	380.6	1313.0	1094.0	1017.3	609.0	1020.2
Ssc.11348.1.A1_at, CO946511, CCT6A	3328.3	3633.6	3890.2	2084.2	2267.7	4866.7	5133.4	3513.2	5731.6	3844.6
Ssc.10287.1.A1_at, BI400474, TGFB2	535.5	680.4	702.3	993.2	445.7	401.2	386.0	328.9	282.6	436.8
Ssc.15146.1.S1_at, CO947014, ICA1	349.7	282.3	247.1	326.5	285.3	145.9	220.2	161.4	167.6	248.0
Ssc.12584.1.A1_at, BI402906, SLC25A29	502.5	726.0	325.3	617.9	518.4	290.6	162.0	458.6	94.1	164.3
Ssc.11819.1.A1_at, BI184969, NAALADL2	286.1	343.2	247.7	330.7	351.5	184.1	157.3	247.4	110.6	339.9
Ssc.27215.1.S1_a_at, CN163568, ALS2CL	1740.4	1415.4	1289.9	2301.7	1942.7	832.3	770.1	1333.0	589.2	1485.8
Ssc.26415.1.A1_at, CN163027, ING3	526.3	585.9	486.2	569.9	498.5	310.5	314.5	355.9	323.5	296.9
Ssc.23827.1.A1_at, CK450783, AGL	1230.6	586.3	941.7	776.1	556.6	726.6	1590.6	980.0	2862.0	993.5

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
50.8	49.5	33.8	64.7	42.4	59.9	271.5	155.2	50.2	45.2	58.1	11.3	0.184810096	0.323429578
30.5	47.1	32.8	44.5	17.5	31.8	163.4	106.0	34.0	68.5	41.5	10.7	0.20830783	0.321008615
32.4	34.6	35.1	28.0	47.3	77.2	77.4	132.3	42.4	22.9	47.0	18.2	0.548234281	0.320638759
22.7	28.4	22.8	27.8	22.0	17.9	42.9	73.7	23.6	17.2	39.7	3.9	0.550373134	0.320304017
1703.5	912.1	1380.2	830.6	557.4	1699.7	2355.3	3691.6	1180.6	589.6	1137.2	482.8	0.501245418	0.319800882
169.9	35.7	41.5	179.3	47.0	52.2	660.2	274.2	87.6	307.3	145.1	67.7	0.132691084	0.319451535
605.1	1037.7	586.7	978.3	334.6	458.0	3382.6	2087.5	666.7	1353.8	831.9	282.4	0.197104431	0.319390154
381.2	146.4	280.5	152.9	226.5	438.3	493.8	849.1	271.0	160.6	250.8	119.7	0.548715456	0.319107175
206.3	74.6	114.8	87.5	65.2	159.9	224.5	370.6	118.1	84.5	118.1	55.1	0.525882038	0.318537507
39.1	30.7	27.2	51.5	28.4	26.4	180.1	106.8	33.9	89.7	30.7	9.8	0.188136221	0.317319098
87.2	179.3	89.5	163.3	42.0	66.3	744.7	330.0	104.6	166.6	132.8	54.7	0.14046679	0.316988908
16.8	44.7	16.3	29.5	24.2	24.7	169.4	82.2	26.0	38.6	14.6	10.4	0.153661512	0.316707218
147.0	240.1	115.6	153.2	114.7	107.3	829.6	463.2	146.3	273.7	163.5	49.6	0.176361635	0.315909549
335.7	340.6	493.1	231.6	718.2	416.1	818.8	1338.7	422.6	341.9	167.9	169.2	0.516060088	0.315646757
194.3	159.7	90.7	184.1	95.3	147.5	912.7	460.3	145.3	328.0	195.9	43.8	0.15916495	0.315604994
19.6	27.6	17.8	24.2	34.3	42.4	158.1	87.8	27.7	36.7	9.6	9.3	0.17493357	0.314992026
111.1	178.8	79.2	127.3	75.4	188.6	655.8	404.7	126.7	145.6	111.7	48.3	0.193244081	0.313153776
396.7	678.7	427.6	525.3	336.5	337.6	3650.0	1442.8	450.4	672.9	343.1	131.8	0.123395908	0.312166452
63.4	115.2	75.9	123.8	101.5	73.3	515.3	296.1	92.2	139.0	36.4	24.8	0.178899498	0.311325003
75.7	193.8	95.6	179.8	79.5	65.1	856.9	369.4	114.9	412.5	192.3	56.7	0.134101182	0.311123746
658.0	800.5	658.5	1076.0	732.8	1457.4	4553.3	2888.2	897.2	1325.5	647.0	315.1	0.197043037	0.310645458
9.8	15.2	15.2	22.4	20.6	12.1	82.0	51.2	15.9	40.3	21.3	4.8	0.193746442	0.310221354
302.3	366.2	426.7	413.2	594.6	962.9	1093.7	1649.4	511.0	486.9	439.0	241.8	0.467214664	0.30980328
79.8	78.3	76.5	47.0	161.5	59.2	154.9	270.5	83.7	107.1	241.1	40.2	0.540316682	0.309534374
68.9	24.4	20.5	14.6	36.4	26.9	200.7	104.0	32.0	89.1	28.6	19.5	0.159224559	0.307152471
154.6	167.3	163.2	114.6	170.8	128.0	297.9	490.1	149.8	127.4	163.9	23.1	0.502719216	0.305537419
29.2	58.0	43.6	98.5	39.4	7.7	324.4	151.0	46.1	145.2	54.9	30.7	0.142005754	0.30503686
163.6	198.9	186.1	103.9	258.9	148.1	360.3	579.3	176.6	105.5	218.3	52.2	0.490128049	0.304832436
175.7	82.1	90.8	109.8	67.9	57.5	170.1	320.9	97.3	56.2	47.9	42.5	0.572083725	0.303209723
96.7	56.2	72.8	46.4	30.1	91.9	141.9	217.2	65.7	50.5	63.1	26.2	0.463015179	0.30238161
526.0	694.6	540.6	342.0	333.1	373.5	969.6	1553.2	468.3	481.1	988.7	143.5	0.482962749	0.301506567
39.1	61.3	46.6	71.9	64.9	19.0	360.2	167.8	50.5	92.5	51.3	19.6	0.140099569	0.30068319
134.1	225.9	104.4	184.3	145.4	135.1	888.9	516.9	154.9	101.8	232.6	43.3	0.174222822	0.299629816
417.6	231.2	242.5	185.1	206.5	464.5	583.7	982.6	291.2	213.4	446.2	118.7	0.498943521	0.296384496
16.8	17.6	25.7	16.8	22.1	22.0	109.6	68.1	20.2	28.8	24.3	3.7	0.183968862	0.296133138
94.3	126.6	92.8	107.4	92.5	92.7	569.2	341.6	101.1	19.1	93.5	13.8	0.177542343	0.295779183
31.5	42.1	46.3	32.2	43.1	72.8	240.1	151.0	44.7	46.0	32.7	15.0	0.18600261	0.295766565
344.6	241.7	329.4	209.4	268.2	475.7	680.3	1055.8	311.5	198.2	298.0	95.4	0.457899688	0.295048117
171.7	221.9	156.2	160.9	165.4	177.0	912.3	595.6	175.5	185.8	23.8	23.9	0.192397635	0.294669039
49.7	93.8	65.6	133.3	37.4	52.3	625.5	244.9	72.0	231.2	102.9	35.7	0.115141922	0.294017583
17.6	47.5	31.7	16.0	22.5	30.1	151.3	93.8	27.6	57.9	19.4	11.7	0.182150566	0.293825055
127.0	170.0	116.6	175.3	131.5	121.1	779.5	477.6	140.3	286.5	175.2	25.7	0.179913795	0.293631187
1378.9	1630.2	1243.4	2166.9	849.1	812.5	7098.5	4604.5	1346.8	1375.1	936.3	509.5	0.189735455	0.292506251
1238.7	678.7	989.4	440.3	548.2	1249.5	1862.0	2935.0	857.5	446.2	1086.2	351.6	0.460518307	0.292156168
299.1	275.5	491.5	257.6	310.3	259.6	699.4	1080.9	315.6	149.4	311.8	88.7	0.451243923	0.291978906
131.2	15.7	31.1	154.9	47.3	22.3	920.9	230.7	67.1	580.4	102.8	60.3	0.072848569	0.29080689
83.5	87.3	69.9	153.4	164.0	51.1	568.0	350.4	101.5	184.5	93.4	46.2	0.178749575	0.289747541
143.2	130.5	126.8	80.9	81.9	159.3	264.3	417.5	120.4	44.4	78.6	32.3	0.455600111	0.288435439
888.9	699.4	848.7	380.1	481.5	929.3	1599.7	2445.3	704.7	380.2	736.8	228.2	0.440499856	0.288160338
36.0	37.2	57.5	38.5	57.2	62.7	111.0	167.6	48.2	45.4	50.3	12.2	0.434005885	0.287558685
127.9	103.4	110.1	59.4	67.5	178.1	205.0	374.8	107.7	61.8	178.5	43.2	0.525528455	0.287426854
705.2	730.0	740.7	350.7	518.9	848.1	1364.9	2259.8	648.9	575.0	458.2	180.9	0.4754578	0.287161514
330.6	149.6	303.0	119.9	382.1	440.9	439.2	1010.7	287.7	103.4	254.9	127.8	0.655016697	0.28463771
1531.5	1275.4	1388.2	863.6	679.3	2147.0	3040.8	4617.9	1314.2	816.7	920.1	520.4	0.432177936	0.284581014
149.3	127.6	119.8	80.5	103.5	43.7	671.4	367.1	104.1	208.6	61.2	37.5	0.154994886	0.283483156
39.8	75.5	52.3	61.1	34.0	57.3	298.2	188.6	53.3	40.3	43.4	15.0	0.178862879	0.282755452
69.5	116.6	84.0	60.3	7.0	59.2	538.0	233.9	66.1	148.8	144.3	35.9	0.122857886	0.282575239
58.8	80.9	39.5	64.9	46.6	60.6	311.8	207.9	58.6	43.8	88.9	14.5	0.187756542	0.281679977
259.0	459.3	293.2	306.0	107.1	268.9	1738.0	1002.1	282.3	407.6	386.2	112.6	0.162397441	0.281664139
110.8	111.7	68.6	76.6	62.0	111.2	533.4	320.3	90.2	43.5	22.1	23.6	0.169022799	0.281490039
316.0	499.3	380.0	256.1	571.8	361.7	818.3	1430.5	397.5	278.1	860.8	117.4	0.485766545	0.277855449

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.30877.1.S1_at, CO955018, AMICA1	356.2	261.8	358.7	612.8	1018.5	181.2	133.9	420.5	102.8	245.3
Ssc.17375.1.S1_at, CF360118, MRAP2	2079.7	2216.7	1659.4	4340.7	3548.1	1395.5	1076.2	2563.2	998.9	1973.3
Ssc.10261.1.A1_at, BI400375, MGAT4A	23.2	67.3	56.5	57.3	81.7	22.4	49.9	39.4	37.6	20.8
Ssc.15629.1.S1_at, BF443163, WDR3	832.2	1032.9	1237.7	551.8	1112.1	1301.7	1701.7	721.9	2606.7	1429.1
Ssc.7528.2.S1_at, AJ660552, HHIP	46.5	51.5	67.7	49.2	103.7	70.9	29.7	50.7	14.8	16.5
Ssc.4266.1.S1_at, CN153874, FERMT1	7179.3	4204.1	7436.1	394.8	1107.2	6212.9	8449.8	2007.3	10616.5	3411.5
Ssc.2264.1.S1_at, CA780403, SLC1A5	3736.7	3596.8	4356.9	1927.4	1909.7	4815.9	6027.1	5070.7	6979.4	4289.7
Ssc.13284.1.A1_at, BI404780, TIAM2	692.9	906.0	999.0	351.0	499.8	2352.1	1057.4	577.8	1077.1	547.7
Ssc.8253.1.A1_at, CK452806, GNL3	1851.3	1850.9	1857.5	794.8	1270.4	2194.5	2872.5	2031.3	4183.8	1960.5
Ssc.13346.1.A1_at, CK463666, FRMD5	819.9	559.1	717.4	931.8	491.7	511.0	1243.4	755.3	2427.4	827.7
Ssc.1756.1.S1_at, BE030832, PDLIM2	213.2	185.4	212.0	451.9	265.4	139.6	153.4	279.9	88.6	185.6
Ssc.2409.1.A1_at, CF368211, FAM13C1	142.6	411.9	108.0	620.4	420.3	242.6	73.1	337.2	34.0	361.5
Ssc.29826.1.A1_at, CO947334, MRPL48	125.6	109.6	75.0	152.7	163.5	79.2	59.3	61.2	80.3	82.9
Ssc.1180.1.S1_at, AW436697, DNAJB2	491.7	372.1	532.1	486.2	463.6	335.1	174.2	418.9	187.4	447.6
Ssc.5710.1.A1_at, BF702013, LRFN5	297.3	452.9	238.9	632.7	602.2	189.8	160.9	244.4	143.4	274.5
Ssc.8569.1.A1_at, BF711966, ADAM5P	11056.1	10493.3	8243.8	10039.0	1148.8	6345.3	6725.0	6746.9	5254.5	8338.2
Ssc.12273.1.A1_at, CN028399, GSTM3	277.8	41.3	52.5	465.8	301.3	902.5	380.8	426.3	908.3	437.3
Ssc.21462.1.S1_at, CF795351, YWHAE	265.1	379.6	355.6	47.5	341.6	637.0	507.7	186.3	468.1	305.7
Ssc.7093.1.A1_at, CB478502, HPSE	113.3	187.6	109.0	232.8	476.8	183.2	104.1	169.0	92.5	144.4
Ssc.7528.1.A1_at, CF359222, HHIP	355.6	243.4	291.0	809.6	610.0	242.4	184.1	245.6	135.3	175.0
Ssc.1496.1.S1_at, BQ603805, NME6	592.8	651.6	488.2	512.8	720.5	346.2	310.5	331.5	261.4	558.3
Ssc.12543.1.A1_at, CO955077, TBC1D7	870.3	792.6	750.2	1038.8	771.2	445.4	315.8	881.9	304.3	803.8
Ssc.13469.1.A1_at, BQ602383, OR5D14	535.2	662.9	441.4	1167.5	777.2	441.0	190.5	588.0	212.9	499.8
Ssc.27153.1.S1_at, BX914539, KIAA0409	490.1	546.1	540.6	384.8	290.0	687.6	706.6	949.6	976.2	626.1
Ssc.10772.1.A1_at, CN162918	307.7	305.3	309.9	280.5	317.7	348.2	578.8	359.8	794.8	288.0
Ssc.11852.1.A1_at, BI185320, ATG10	262.6	201.2	188.0	294.5	288.0	116.7	154.4	158.2	74.6	163.5
Ssc.15829.1.S1_at, BP148315, RARA	60.2	32.9	59.0	36.1	16.4	85.1	52.7	35.8	89.7	68.8
Ssc.17299.2.S1_at, CA781065, MTMR11	654.3	994.9	1464.7	376.5	465.8	579.2	495.9	307.6	349.0	548.0
Ssc.24214.1.S1_at, CK452635, GRWD1	1017.0	766.6	1021.9	420.7	540.2	1059.6	1169.2	964.2	1782.0	819.0
Ssc.26482.1.A1_at, CN155726, ECHDC2	516.0	498.2	391.3	747.4	751.8	408.3	375.0	467.3	222.4	327.1
Ssc.9291.1.A1_at, BF710122, PALMD	1058.2	877.3	516.2	699.2	958.6	337.2	471.5	490.8	401.9	853.0
Ssc.23054.1.S1_at, BX673669, JAK3	1257.2	1264.1	1005.5	1945.3	1711.2	706.7	725.0	832.3	506.3	574.3
Ssc.5281.1.A1_at, BQ599136, WDR12	458.0	417.3	488.0	315.5	316.7	555.7	970.0	473.9	1198.8	435.2
Ssc.19546.1.S1_at, CK459631, NME1	2291.4	1984.8	3356.9	878.7	1166.6	2599.4	3585.1	3602.4	2633.6	2260.2
Ssc.5362.2.S1_at, BP138196, NEK6	128.0	148.4	185.4	66.0	197.0	331.3	261.2	113.9	281.5	195.0
Ssc.29282.1.A1_at, CO952240, RGS3	413.5	359.6	181.0	245.0	296.1	485.4	417.1	538.4	564.6	386.5
Ssc.30418.1.A1_at, CO991645, ASTN2	247.5	59.0	575.9	113.7	188.4	355.3	877.1	242.8	894.4	154.4
Ssc.10430.1.A1_at, CK452419, PAPSS2	210.1	140.5	365.2	218.5	307.3	636.7	551.2	260.5	290.4	292.3
Ssc.8528.2.S1_at, BX916654, CTSC	783.9	862.4	1480.8	400.0	841.6	1225.9	1500.8	669.2	1749.0	1582.8
Ssc.22140.1.S1_at, CN160603, TET2	178.9	48.9	67.5	89.9	174.2	218.5	329.4	134.9	428.8	157.4
Ssc.10108.1.A1_at, CF175360, NKAIN2	456.4	562.3	367.3	553.6	560.6	264.5	180.2	325.9	236.0	321.6
Ssc.8063.1.A1_at, CK452230, RBM47	138.8	126.0	167.9	183.9	261.8	153.2	93.7	114.0	69.8	129.4
Ssc.29500.1.A1_at, CO940428, NPAL2	492.4	795.2	498.3	572.9	917.9	451.7	229.4	367.1	141.5	499.8
Ssc.26079.1.S1_at, BX918995, C10orf91	549.7	439.0	825.2	556.2	401.3	825.6	814.4	1108.7	1330.2	906.5
Ssc.24381.1.S1_at, CN164362, PIGX	801.2	824.2	977.5	1297.0	823.1	241.9	760.1	935.0	415.4	776.0
Ssc.28870.1.S1_at, CO986782	278.7	354.8	244.8	582.0	315.8	226.3	173.7	210.2	124.3	255.7
Ssc.24912.1.S1_at, BE236119, RRP12	1034.1	752.5	1048.0	382.9	475.9	947.8	1190.5	1132.0	1816.1	792.4
Ssc.30690.1.A1_at, CO945134, PPRC1	1108.9	861.0	1140.3	1022.3	545.5	871.2	1389.4	1663.2	2450.1	1205.2
Ssc.3391.1.S1_at, BI400819, FOSL1	833.3	333.6	714.2	101.7	69.8	543.0	769.0	675.3	1895.8	372.3
Ssc.18584.1.A1_at, CK462034, NT5C1B	175.5	193.5	194.1	191.1	194.7	181.4	190.9	77.6	76.5	49.1
Ssc.1450.1.S1_at, CK465052, SRM	3032.6	2111.3	3386.3	1053.8	1436.5	3590.2	4271.0	3077.8	5627.4	2488.7
Ssc.9408.1.S1_at, CO953576, CC2D1B	381.7	301.8	250.7	396.5	431.9	207.5	202.7	313.6	120.8	255.5
Ssc.14311.1.A1_at, CF363329, KIAA1407	89.7	158.6	88.7	182.9	191.0	110.9	83.3	84.7	53.7	92.0
Ssc.8868.1.S1_at, BX926353, FCGR2B	138.9	226.9	113.5	323.5	791.5	270.0	125.5	166.9	67.3	138.4
Ssc.8980.1.A1_at, BI183736, ANGPTL4	361.0	341.5	352.5	378.0	55.3	702.3	992.1	485.6	573.7	456.5
Ssc.30245.1.A1_s_at, CO988922	283.9	254.6	293.5	656.7	351.2	115.3	134.8	203.2	103.0	337.7
Ssc.6196.1.S1_at, CK451068, NPM3	2757.4	1945.2	2836.5	717.4	784.9	2221.7	2967.6	2748.7	4449.5	2379.8
Ssc.21597.1.S1_at, CN166138, DKC1	1396.4	1246.4	1518.6	466.1	725.8	1432.1	2005.8	1510.5	3170.0	1340.5
Ssc.27359.1.S1_at, CN156418	136.1	146.9	102.8	190.0	233.7	84.7	101.8	118.4	50.5	76.2
Ssc.11117.1.A1_at, BI181891, PDE1B	4237.6	2595.3	5175.2	1207.0	1804.5	3878.7	6482.3	4286.1	7675.4	4425.7
Ssc.30366.1.A1_at, CO990838, ATXN7L1	328.4	292.6	340.0	473.8	464.7	147.2	208.5	421.6	188.4	220.6

Appendix (online only). Continued

VPA						*Pixel intensity*							
						Average			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
88.4	18.2	38.8	126.0	52.2	37.7	521.6	216.7	60.2	306.8	125.9	39.8	0.115446063	0.277829042
394.5	809.7	341.4	480.8	401.7	230.9	2768.9	1601.4	443.2	1127.9	660.4	197.6	0.160050369	0.276733566
3.5	19.7	6.4	10.1	8.9	7.7	57.2	34.0	9.4	21.6	12.3	5.5	0.164044289	0.275818146
770.3	373.9	371.5	317.7	239.5	491.0	953.3	1552.2	427.3	268.5	689.5	187.1	0.448231131	0.27529388
19.9	3.0	6.8	17.3	12.5	0.7	63.7	36.5	10.0	23.8	24.0	7.8	0.15745972	0.274735305
1621.9	914.0	1991.2	192.4	431.5	4907.9	4064.3	6139.6	1676.5	3290.2	3532.1	1725.0	0.412490056	0.273060677
1886.1	1280.6	1837.1	829.8	1057.3	1990.1	3105.5	5436.6	1480.2	1120.7	1068.1	488.6	0.476627489	0.272261626
200.0	256.0	418.6	65.7	310.4	573.7	689.7	1122.4	304.1	270.8	732.3	176.5	0.440842443	0.270902752
900.2	528.9	805.1	415.0	466.8	1172.1	1525.0	2648.5	714.7	479.9	931.1	295.8	0.468650955	0.269842528
258.3	394.8	320.2	203.8	437.1	249.9	704.0	1153.0	310.7	181.4	759.7	90.6	0.441324091	0.269465839
35.6	64.6	37.2	52.3	56.7	27.5	265.6	169.4	45.7	108.1	71.0	14.3	0.171887943	0.269448707
41.9	84.0	68.9	78.6	27.9	35.2	340.6	209.7	56.1	213.9	149.9	24.0	0.164641068	0.267471067
12.1	18.7	10.4	20.3	7.5	47.2	125.3	72.6	19.4	35.3	11.4	14.5	0.154587058	0.266832001
81.9	81.0	103.8	77.3	51.7	99.6	469.1	312.6	82.6	59.6	127.3	18.6	0.175960268	0.264041709
77.7	92.4	39.8	63.7	27.7	19.3	444.8	202.6	53.4	176.3	55.5	29.1	0.120128897	0.263738072
1733.7	2399.6	1660.3	2661.5	1451.3	667.01	0196.2	6682.0	1762.2	1180.2	1106.8	710.3	0.172832362	0.263729214
174.6	249.6	240.8	75.6	153.2	73.0	227.7	611.0	161.1	180.3	269.6	76.8	0.707531981	0.263703413
102.7	89.0	84.6	114.3	96.1	179.0	277.9	421.0	111.0	135.7	176.6	34.9	0.399273068	0.263564234
52.6	15.0	39.6	83.9	20.2	7.2	223.9	138.6	36.4	150.7	39.6	28.6	0.162647015	0.262670706
50.5	61.6	42.5	61.8	57.2	35.4	461.9	196.5	51.5	240.4	47.1	10.8	0.111491167	0.262113192
102.4	67.0	125.5	85.6	69.6	118.5	593.2	361.6	94.8	96.3	114.5	24.7	0.159760388	0.262090455
214.4	142.2	133.5	132.9	83.1	155.4	844.6	550.2	143.6	117.7	274.2	42.5	0.169997553	0.260946738
140.2	106.8	84.7	170.0	54.5	45.4	716.8	386.4	100.3	282.2	176.8	48.7	0.139873147	0.259462444
256.9	170.3	281.7	155.0	135.0	224.5	450.3	789.2	203.9	110.6	161.6	59.3	0.452789128	0.258356352
130.0	108.1	118.3	61.6	84.8	230.3	304.2	473.9	122.2	14.1	210.6	58.4	0.401628208	0.257814258
36.9	55.9	21.7	39.4	20.2	30.3	246.9	133.5	34.1	49.4	37.7	13.2	0.137999946	0.255219259
26.6	19.6	15.9	12.8	11.5	15.3	40.9	66.4	17.0	18.6	22.5	5.5	0.414222874	0.255194219
117.1	108.0	49.1	89.0	103.4	226.9	791.2	455.9	115.6	444.9	121.1	59.5	0.146078729	0.253505578
425.0	213.8	354.6	169.8	175.7	417.9	753.3	1158.8	292.8	272.9	371.4	120.0	0.388700085	0.252675181
68.7	123.8	86.5	87.7	113.9	64.9	580.9	360.0	90.9	161.2	92.3	23.7	0.156499237	0.252532267
155.9	189.4	93.2	126.1	103.3	100.3	821.9	510.9	128.0	215.7	200.6	37.8	0.155777264	0.250613321
168.1	265.7	139.5	161.1	110.8	158.3	1436.7	668.9	167.3	381.4	129.1	52.5	0.116415853	0.250029899
265.8	97.4	197.7	100.6	114.0	314.4	399.1	726.7	181.7	79.8	339.2	93.0	0.455149085	0.249958719
893.3	474.5	815.1	391.0	642.9	1162.8	1935.7	2936.1	729.9	982.0	617.8	286.0	0.37709401	0.248603041
75.4	50.8	68.0	37.5	46.7	73.2	145.0	236.6	58.6	52.1	84.2	15.7	0.404249448	0.24769634
167.1	133.1	145.0	63.1	58.3	143.8	299.0	478.4	118.4	91.7	76.3	46.1	0.395933654	0.247491639
87.3	83.8	257.5	124.5	78.1	112.4	236.9	504.8	123.9	202.6	355.0	67.9	0.523146194	0.245509773
73.3	106.1	74.7	51.3	143.1	149.8	248.3	406.2	99.7	88.2	174.5	40.2	0.401565185	0.245474538
367.0	246.7	268.2	171.4	131.6	796.7	873.7	1345.5	330.3	388.0	422.8	242.7	0.377991927	0.245452879
75.1	63.4	63.6	60.9	29.3	81.1	111.9	253.8	62.2	60.8	123.5	18.0	0.556250745	0.245206199
48.0	99.3	50.4	71.5	73.7	45.4	500.0	265.6	64.7	86.5	61.1	20.9	0.129422979	0.243625458
62.4	3.3	16.8	47.8	13.6	19.8	175.7	112.0	27.3	53.3	32.1	22.7	0.155301305	0.243557698
127.2	88.2	72.7	133.2	37.5	34.7	655.3	337.9	82.3	191.4	150.3	42.4	0.12550737	0.243415212
185.8	175.1	281.0	284.3	198.3	322.1	554.3	997.1	241.1	165.9	220.5	62.1	0.434978711	0.241806074
173.7	119.2	125.4	89.3	110.1	280.1	944.6	625.7	149.6	209.2	286.3	69.7	0.158409203	0.239153135
46.2	43.4	38.3	44.3	41.9	69.6	355.2	198.0	47.3	133.3	50.7	11.3	0.133109998	0.23875648
411.9	212.4	327.4	143.6	150.1	420.5	738.7	1175.8	277.7	307.7	390.9	126.0	0.375873179	0.236145132
392.1	376.2	370.6	340.2	316.5	349.7	935.6	1515.8	357.6	243.5	596.4	27.4	0.38216118	0.23587893
304.6	66.8	272.0	32.8	128.4	399.8	410.5	851.1	200.7	349.4	602.7	146.2	0.488973335	0.235857185
27.3	21.3	28.4	25.9	22.2	37.7	189.8	115.1	27.1	8.1	65.9	5.9	0.142972565	0.23573704
1225.8	749.0	1017.3	499.3	465.0	1429.2	2204.1	3811.0	897.6	1000.6	1208.9	393.1	0.407241051	0.235527497
49.5	59.4	47.5	64.6	44.0	45.2	352.5	220.0	51.7	74.2	71.3	8.4	0.146658346	0.234978638
13.3	36.6	12.7	28.5	6.2	22.4	142.2	84.9	20.0	49.8	20.6	11.3	0.140315094	0.23492699
59.4	16.5	20.2	91.4	9.4	18.8	318.9	153.6	36.0	276.8	74.5	32.4	0.112745406	0.234019008
166.6	58.7	198.4	29.1	231.1	216.8	297.7	642.0	150.1	136.1	217.8	85.6	0.504322605	0.233812016
42.0	87.5	16.1	66.9	19.3	18.9	368.0	178.8	41.8	165.2	96.9	29.7	0.113547838	0.233687547
893.2	570.7	763.6	369.3	366.6	1146.9	1808.3	2953.5	685.1	1026.4	886.7	308.9	0.378840666	0.231948291
633.0	331.5	496.0	324.6	237.6	578.1	1070.7	1891.8	433.5	453.3	759.5	158.3	0.404859308	0.229131647
15.7	25.1	18.8	25.1	17.9	15.9	161.9	86.3	19.8	50.8	25.8	4.3	0.121988882	0.228799815
1479.4	690.7	1714.4	689.9	817.3	1910.0	3003.9	5349.6	1217.0	1663.6	1646.2	549.7	0.405120642	0.227482597
51.2	95.4	35.5	62.0	41.5	34.8	379.9	237.3	53.4	83.5	106.8	23.0	0.140563306	0.225069544

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.6425.3.A1_at, BI399085, ABCC5	431.7	295.7	409.9	596.9	561.5	286.7	219.9	329.6	128.9	263.8
Ssc.14190.1.A1_at, BQ600716, KLHL1	67.2	46.9	36.7	36.8	46.1	61.3	58.0	54.4	79.9	116.8
Ssc.9720.1.A1_at, CF365800, CYR61	2848.3	2697.8	2555.8	4148.3	2296.9	4171.0	7710.5	9619.9	4315.2	5048.3
Ssc.22390.1.A1_at, CF792574	184.1	213.4	169.1	139.8	243.3	84.5	78.3	108.0	117.1	175.1
Ssc.16663.1.S1_at, CN162878, ITGA5	4353.3	3376.7	5324.6	2643.5	2913.1	5947.0	5574.5	4617.2	6282.6	5937.1
Ssc.12616.1.A1_at, BI403019, CYP1B1	157.0	248.9	275.8	91.4	83.6	242.9	384.5	386.7	238.7	233.0
Ssc.21077.1.S1_at, BX676555, C10orf32	464.9	567.0	439.6	689.2	738.5	310.9	326.4	439.7	252.5	378.4
Ssc.17299.1.A1_at, BI185005, MTMR11	1599.2	2072.7	2581.5	1306.2	934.5	1096.0	1059.6	762.6	997.4	1431.3
Ssc.13347.1.A1_at, BI404879, CADM2	205.9	166.8	112.4	321.0	274.7	72.9	52.7	120.1	55.8	123.8
Ssc.5258.1.A1_at, BI182081, AATF	705.6	639.1	629.8	357.5	487.2	852.3	952.2	770.5	1364.4	732.2
Ssc.719.1.S1_at, NM_213876.1, CXCL6	31.4	38.4	90.3	58.1	26.8	33.0	130.0	53.7	116.2	54.2
Ssc.25125.1.S1_at, CK463916, BMPER	985.1	709.0	581.5	722.7	852.0	345.5	589.9	439.7	422.6	352.4
Ssc.8355.1.A1_at, BF712614, KIAA1598	164.4	291.3	144.1	444.5	426.0	136.7	37.3	125.0	95.3	177.3
Ssc.29038.1.A1_at, CO990936, MBNL3	442.7	289.0	379.2	842.1	810.6	285.1	225.9	395.8	176.0	232.5
Ssc.21195.1.S1_at, CN166161, PERLD1	306.0	289.0	224.8	299.0	296.7	184.3	111.9	112.6	148.8	180.4
Ssc.10453.1.S1_at, BF713714, CP	314.2	793.0	433.5	1292.2	777.4	315.3	330.7	459.6	90.3	137.8
Ssc.30823.2.A1_at, CO943599, ABI3BP	3593.5	3666.1	4598.0	2838.9	2552.1	5084.9	5481.3	4882.0	6628.7	4302.9
Ssc.9663.1.A1_at, BF711181, FAM78B	439.8	328.5	285.8	520.3	214.4	164.1	188.8	299.3	139.1	228.0
Ssc.25069.1.S1_at, CN153765, CTPS	568.3	436.3	700.3	199.9	293.5	565.6	858.8	827.2	1018.4	584.9
Ssc.17029.1.A1_at, CK456293, ABO	81.1	136.1	71.9	83.2	115.7	217.6	115.0	16.6	109.9	292.6
Ssc.8528.3.S1_at, CB469613, CTSC	325.0	255.1	521.1	352.4	346.0	296.4	579.8	454.8	781.0	721.2
Ssc.24152.1.A1_at, CK456890, SMAD6	2588.2	4668.6	2547.2	3333.8	3231.0	4528.1	5288.5	5886.2	4651.7	5502.7
Ssc.27391.1.S1_at, BI346183, TP53I3	242.0	127.8	193.2	211.3	132.9	76.6	105.4	119.7	104.9	165.3
Ssc.3088.1.S1_at, CN166193, MRC2	620.6	387.4	728.2	217.1	216.0	846.6	1285.3	863.4	1996.8	625.4
Ssc.1609.1.A1_at, CF368424	3676.5	2041.2	2746.6	2492.0	3035.5	991.5	2034.4	1898.3	1738.3	2458.9
Ssc.8587.1.S1_at, CK451144, CETN3	1589.7	1579.8	1099.2	2461.2	1710.7	1426.5	884.2	1355.7	524.5	1371.6
Ssc.10406.1.A1_at, BI400960, THBS1	309.9	1119.2	544.7	559.3	428.7	691.7	644.3	4449.0	784.6	487.5
Ssc.15114.1.S1_at, CN159011	855.3	874.9	1025.8	571.9	744.9	1130.9	1637.1	965.6	1671.9	908.7
Ssc.16342.1.A1_at, NM_214287.1, SERPINE2	4261.2	3975.6	6090.2	2323.7	1735.1	6788.2	5138.4	4779.7	8510.6	5438.8
Ssc.10601.1.A1_at, BM190013, PICALM	62.9	112.6	69.3	86.9	124.3	87.6	41.8	60.0	37.4	75.6
Ssc.7334.1.A1_at, BF703666	145.1	98.7	73.2	96.4	157.5	34.1	55.7	82.1	59.6	72.1
Ssc.30919.1.A1_at, CO944279, MYST4	969.4	915.7	780.6	1752.1	1255.7	563.8	679.1	595.2	373.6	618.0
Ssc.16297.1.S2_at, NM_214268.1, SELE	850.6	823.4	866.7	544.6	359.4	316.4	1893.9	960.2	1370.4	736.0
Ssc.25108.1.A1_a_at, CK466113, TJP2	230.5	280.6	238.9	160.6	147.9	294.9	325.0	179.5	542.4	272.3
Ssc.11991.1.A1_at, BI184429, CD163	315.4	257.0	150.1	544.5	1024.9	92.1	148.8	561.1	146.7	124.0
Ssc.24490.1.S1_at, CN155314, ELOVL5	307.9	244.0	177.1	220.5	172.0	256.4	617.6	143.4	1169.5	313.7
Ssc.6323.1.S1_at, AY550037.1, ADFP	397.5	331.5	516.1	346.0	310.8	473.4	777.6	741.9	608.7	465.5
Ssc.18572.1.S1_at, CN153410, GPNMB	429.9	202.0	388.6	678.7	495.1	114.5	179.7	537.0	128.0	179.9
Ssc.2516.3.S1_a_at, CK457480, SLC5A6	1856.8	1375.1	2222.8	891.9	1107.3	2158.2	2629.9	2109.2	3148.9	2002.2
Ssc.26456.1.A1_at, CN069543, C17orf60	121.3	107.9	40.7	330.3	263.0	46.0	45.8	97.7	34.5	66.2
Ssc.23766.1.S1_at, CO946863, PHF15	1537.6	1058.2	1826.4	1346.7	1119.8	813.9	875.5	774.2	515.7	1175.7
Ssc.21930.1.S1_a_at, CK452448, ISOC2	1098.9	721.3	684.7	773.2	939.0	511.7	351.8	526.4	384.6	617.7
Ssc.2516.2.S1_a_at, CN158396, SLC5A6	868.3	704.3	920.8	245.4	574.5	1163.0	1236.6	601.9	1764.6	914.6
Ssc.24250.1.S1_at, CN160216, CRABP2	85.7	74.0	48.1	119.7	135.4	253.3	58.3	188.5	55.7	289.9
Ssc.4669.1.S1_at, BI342019, NIPBL	1227.9	1086.1	1170.8	1883.5	1359.6	787.3	683.7	1373.8	496.3	843.5
Ssc.21935.1.S1_at, CN159935, TNS3	1550.6	841.6	1974.3	1526.6	1296.5	1051.2	663.0	366.6	914.1	694.7
Ssc.8528.1.A1_at, BF704096, CTSC	1346.1	1093.9	1079.8	1419.4	1544.4	1013.2	2333.3	1638.0	3289.9	1983.7
Ssc.4681.1.S1_at, BF077805, CD93	442.5	391.9	631.9	546.9	851.6	1087.4	882.4	996.1	1468.4	963.5
Ssc.11060.1.S1_at, AW359493, BOP1	3140.6	3906.4	2433.5	4065.0	7227.8	1524.3	1291.0	4028.8	783.6	1770.1
Ssc.2362.1.S1_at, BI181772, SLCO2B1	338.1	273.3	217.3	473.5	626.7	199.0	112.2	186.1	86.5	122.9
Ssc.10766.1.A1_at, BQ597923, RNF135	471.4	470.1	339.6	459.5	453.6	287.0	221.9	251.3	189.0	358.4
Ssc.30998.1.A1_at, CK459414, RCBTB2	1395.0	1405.7	983.4	1606.9	1692.3	1156.5	836.2	868.0	497.1	1304.6
Ssc.8562.2.S1_a_at, U83916.1, CTGF	1237.1	1345.2	818.9	176.7	1470.5	1404.8	3247.1	1006.5	1567.2	695.8
Ssc.17522.1.A1_at, CO993758, ALDH1A2	1419.3	3317.9	2454.9	5547.2	2679.2	1523.6	1048.1	1614.3	895.7	2270.3
Ssc.21626.2.S1_at, CF787451, GAS1	1582.9	1428.7	1615.9	508.4	1245.7	661.6	633.2	426.7	512.7	770.2
Ssc.7907.1.A1_at, BI181465, ST6GAL1	2595.3	2347.4	2393.5	3777.4	4827.2	1888.9	1912.3	2456.3	1145.0	3018.9
Ssc.30925.1.A1_at, CO956747, DKK2	57.4	66.8	94.2	204.5	114.5	102.8	531.5	101.1	65.5	99.0
Ssc.10650.1.A1_at, AJ660919	1741.9	1455.4	718.3	1594.1	1441.4	739.7	893.5	596.5	978.3	635.8
Ssc.10505.1.A1_at, CF179415, EPC1	1516.4	1523.9	1076.2	1513.3	1716.4	778.5	998.0	967.7	970.5	1049.1
Ssc.18737.1.S1_at, BX923499, LETM1	394.2	474.2	538.7	171.5	305.5	714.1	906.3	486.3	1025.2	429.9
Ssc.11361.1.S1_at, BI401143, C4orf18	1758.4	2037.2	1575.0	1980.4	1484.1	1220.1	934.5	863.4	791.8	1303.6

Appendix (online only). Continued

VPA						*Pixel intensity*						*Ratio*	
						Average			*Standard deviation*				
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
45.2	62.5	49.0	70.0	50.0	55.0	459.1	245.8	55.3	121.8	76.4	9.4	0.120406267	0.224930154
32.4	9.4	13.3	14.4	16.7	13.3	46.7	74.1	16.6	12.4	25.8	8.1	0.354799601	0.223857091
1504.5	1377.1	703.4	1092.5	2138.2	1329.0	2909.4	6173.0	1357.5	721.7	2396.3	475.5	0.466570657	0.219901895
30.5	26.0	18.5	30.5	30.5	11.5	189.9	112.6	24.6	39.9	38.5	7.9	0.129426837	0.218324452
1336.4	1221.8	1383.6	638.1	1163.1	1644.7	3722.2	5671.7	1231.3	1107.2	640.5	335.2	0.330790957	0.21709323
50.4	31.9	36.0	17.3	23.5	227.4	171.3	297.2	64.4	88.3	80.8	80.6	0.375958134	0.216774353
58.9	95.8	76.2	87.1	75.6	48.2	579.8	341.6	73.6	132.5	70.9	17.6	0.126989054	0.215566876
263.5	193.8	147.5	139.0	210.8	414.2	1698.8	1069.4	228.1	645.6	240.4	101.8	0.134289291	0.213332336
18.5	23.8	10.9	18.5	17.7	18.2	216.2	85.1	17.9	83.3	34.6	4.1	0.082963237	0.21083157
271.3	167.8	203.7	110.3	116.7	309.5	563.8	934.3	196.6	140.1	254.8	81.3	0.348591799	0.210366898
9.0	11.3	5.2	12.8	10.2	48.7	49.0	77.4	16.2	26.0	42.8	16.1	0.330612245	0.209248256
85.2	143.1	99.2	86.3	61.9	62.9	770.1	430.0	89.8	153.7	98.6	29.9	0.116571003	0.208749981
36.4	17.9	9.7	36.6	13.3	28.3	294.1	114.3	23.7	140.8	52.1	11.7	0.080595797	0.207312806
61.4	25.2	45.8	87.8	76.3	29.9	552.7	263.1	54.4	255.9	83.7	25.2	0.098422348	0.206796928
33.9	22.4	29.0	28.3	31.6	37.8	283.1	147.6	30.5	33.2	35.1	5.3	0.107735782	0.206639566
60.4	38.3	88.5	45.4	65.3	32.6	722.1	266.7	55.1	381.7	151.2	20.6	0.076286366	0.206505711
1451.5	863.7	1305.3	900.6	659.8	1343.6	3449.7	5276.0	1087.4	800.8	867.6	320.5	0.31521882	0.20610783
34.2	65.7	45.9	52.0	22.6	31.2	357.8	203.9	41.9	122.2	62.6	15.7	0.117210793	0.20569672
175.8	132.1	185.1	81.7	119.4	254.6	439.7	771.0	158.1	202.1	192.9	60.6	0.35963396	0.205085303
37.7	19.6	29.4	70.5	13.1	14.5	97.6	150.3	30.8	27.2	106.7	21.6	0.31557377	0.204868964
85.1	71.8	52.3	63.9	81.2	338.8	359.9	566.6	115.5	98.0	197.2	110.0	0.320950952	0.203862535
1002.0	1619.2	981.4	1455.7	699.6	566.6	3273.8	5171.4	1054.1	858.6	574.1	412.8	0.321979416	0.203827818
25.9	28.0	25.0	14.6	24.6	20.0	181.4	114.4	23.0	49.8	32.5	4.9	0.126855526	0.201229819
317.1	138.4	312.9	69.9	246.3	266.1	433.9	1123.5	225.1	233.5	543.4	99.9	0.518869374	0.200370865
558.1	436.5	465.2	215.6	163.1	354.4	2798.4	1824.3	365.5	611.8	537.0	152.1	0.13060626	0.20034388
215.4	302.6	148.1	262.0	107.5	293.2	1688.1	1112.5	221.5	491.5	394.6	79.7	0.131191306	0.199071161
52.3	407.6	260.9	125.1	551.3	280.0	592.4	1411.4	279.5	311.2	1701.5	182.3	0.47189772	0.198051135
334.0	205.6	283.0	191.1	189.9	287.4	814.6	1262.8	248.5	168.6	366.9	61.0	0.305072677	0.196778689
1375.9	760.0	1625.3	547.8	1339.2	1474.6	3677.2	6131.1	1187.1	1721.7	1531.7	430.0	0.322839728	0.193623589
17.8	1.3	8.5	16.0	13.8	10.7	91.2	60.5	11.4	26.7	21.5	6.0	0.124451754	0.187665344
5.8	13.1	13.5	10.8	11.8	11.5	114.2	60.7	11.1	35.6	18.2	2.8	0.097068955	0.18253184
90.8	168.6	75.5	77.8	84.5	114.4	1134.7	565.9	101.9	386.2	115.5	35.5	0.089832849	0.180113322
58.6	21.1	19.7	26.3	36.6	977.0	688.9	1055.4	189.9	226.5	604.1	385.9	0.275616648	0.179919397
63.1	58.1	80.6	31.4	32.7	82.2	211.7	322.8	58.0	56.0	134.3	22.2	0.27405133	0.179718316
36.9	9.2	19.7	134.0	18.0	10.0	458.4	214.5	38.0	348.0	195.1	48.1	0.08282793	0.176967776
84.8	77.5	100.1	74.0	48.3	145.0	224.3	500.1	88.3	55.6	413.3	32.5	0.393594888	0.176524301
137.5	76.6	127.9	66.9	76.8	160.7	380.4	613.4	107.7	82.3	145.7	39.2	0.283225546	0.175627357
86.9	18.9	19.8	83.0	11.9	18.3	438.9	227.8	39.8	172.8	175.4	35.1	0.090689514	0.174699324
443.5	290.6	469.8	228.5	314.2	760.2	1490.8	2409.7	417.8	545.2	478.2	191.5	0.280255973	0.173384018
16.0	4.5	12.0	18.1	5.9	3.2	172.6	58.0	10.0	119.6	24.9	6.3	0.057634384	0.171433494
138.7	149.4	121.5	133.9	154.3	142.1	1377.7	831.0	140.0	314.8	236.5	11.6	0.101603592	0.168451665
53.4	86.0	100.3	86.2	36.5	114.9	843.4	478.4	79.6	172.8	109.1	29.3	0.09431837	0.166269543
196.5	167.9	173.4	130.1	180.3	267.6	662.7	1136.1	186.0	270.4	430.2	45.6	0.280636626	0.163682879
35.0	16.0	42.7	23.0	8.9	37.6	92.6	169.1	27.2	35.1	108.6	13.3	0.293799957	0.160813527
133.0	169.1	112.6	155.1	107.6	123.5	1345.6	836.9	133.5	316.7	328.0	24.3	0.099201336	0.15949354
132.6	199.1	69.2	116.6	114.3	74.0	1437.9	737.9	117.6	413.5	262.0	47.2	0.081807982	0.159412041
239.3	185.0	379.8	224.5	310.9	591.3	1296.7	2051.6	321.8	204.3	846.6	149.1	0.2481646	0.156851659
190.4	108.5	191.2	108.5	164.3	240.0	573.0	1079.6	167.2	181.4	229.4	51.6	0.291730662	0.154831598
371.5	239.3	178.8	553.0	226.9	151.7	4154.7	1879.6	286.9	1837.4	1255.5	150.9	0.069046966	0.152624373
13.8	21.4	19.2	44.6	16.4	13.5	385.8	141.3	21.5	165.1	48.8	11.7	0.055688043	0.151997547
41.7	56.8	35.2	50.5	15.7	35.2	438.8	261.5	39.2	56.0	65.1	14.3	0.089288427	0.149829204
136.8	151.3	112.1	149.6	85.4	172.3	1416.7	932.5	134.6	274.1	312.9	31.2	0.095000447	0.144328386
263.4	123.7	111.1	345.6	383.6	126.9	1009.7	1584.3	225.7	526.0	990.0	121.7	0.223552677	0.142472711
365.0	363.9	155.6	113.4	149.0	97.6	3083.7	1470.4	207.4	1537.3	541.3	123.5	0.067262272	0.141061389
111.3	106.4	95.8	47.5	114.4	31.8	1276.3	600.9	84.5	453.6	133.7	35.7	0.066232084	0.140682554
233.1	401.5	186.3	362.7	287.4	245.5	3188.2	2084.3	286.1	1086.7	700.3	82.0	0.089733054	0.13725763
43.0	20.6	12.4	19.6	26.5	25.4	107.5	180.0	24.6	58.7	197.1	10.3	0.228724724	0.136589251
61.6	165.9	66.9	116.6	93.2	104.0	1390.2	768.8	101.4	394.8	164.1	38.1	0.072914119	0.131857363
133.7	131.0	117.5	135.2	127.7	92.1	1469.2	952.8	122.9	236.0	102.8	16.3	0.083626002	0.128958674
131.2	103.4	86.2	57.4	70.2	101.9	376.8	712.4	91.7	144.3	258.1	26.3	0.243396493	0.128750445
114.0	207.0	103.5	184.3	111.6	63.1	1767.0	1022.7	130.6	242.7	226.0	54.1	0.073900314	0.127687383

Appendix (online only). Continued

	Sham					*Control-injury*				
Gene	*1*	*2*	*3*	*4*	*5*	*1*	*2*	*3*	*4*	*5*
Ssc.24631.1.S1_at, CK461650, C12orf64	70.1	122.4	58.8	199.4	180.9	124.8	50.7	127.0	26.5	39.5
Ssc.5204.1.S1_at, CK463412, CDA	2549.1	1608.0	2754.8	491.6	826.9	2969.2	3127.7	1840.1	4040.7	2247.0
Ssc.9594.1.A1_at, BI186412, MTHFD1L	521.0	441.5	697.0	113.7	263.3	446.8	1002.5	620.5	934.4	474.0
Ssc.21866.1.S1_at, BX925425, EPB49	422.8	411.6	665.6	218.1	256.7	1763.1	306.6	240.6	248.8	407.8
Ssc.5053.1.S1_at, NM_213976.1, CD163	1339.7	1338.6	1229.1	3249.5	4054.1	841.4	758.8	1246.2	343.7	999.6
Ssc.29441.1.A1_at, CO955541, C13orf33	259.5	653.0	852.3	906.2	790.3	2474.7	693.4	1441.9	4904.4	2096.0
Ssc.21626.1.A1_at, CF788044, GAS1	5199.6	3473.8	4054.0	2334.9	2633.0	1660.7	1856.0	2085.1	1726.3	2542.5
Ssc.12790.1.A1_at, BI404162, VEGFC	275.8	86.8	195.0	80.9	60.0	186.2	279.8	233.3	335.9	236.6
Ssc.3909.1.A1_at, BQ600255, SLC16A9	3332.9	6118.2	1724.8	4616.4	7473.6	1120.6	2349.5	2330.1	798.4	2747.3
Ssc.29841.1.A1_s_at, CO937361	70.0	231.6	67.4	88.4	157.0	693.0	452.5	104.9	838.2	559.9

Appendix (online only). Continued

						Pixel intensity							
VPA						*Average*			*Standard deviation*			*Ratio*	
1	*2*	*3*	*4*	*5*	*6*	*Sham*	*Injury*	*VPA*	*Sham*	*Injury*	*VPA*	*Sham/VPA*	*Injury/VPA*
16.0	7.4	6.3	9.3	5.8	9.2	126.3	73.7	9.0	63.4	48.4	3.7	0.071247625	0.122116689
396.0	253.8	344.8	184.8	120.9	690.2	1646.1	2844.9	331.8	1006.2	850.4	202.4	0.201539415	0.116610544
97.5	28.5	87.4	59.7	62.3	137.3	407.3	695.6	78.8	226.4	258.8	37.5	0.193428267	0.113253024
70.5	65.3	72.7	44.6	51.9	67.8	395.0	593.4	62.1	176.6	657.3	11.3	0.157315509	0.104710865
214.2	31.1	21.6	180.4	52.0	10.7	2242.2	837.9	85.0	1318.6	332.9	88.7	0.037909196	0.101439244
206.4	205.9	204.2	182.7	406.4	191.7	692.3	2322.1	232.9	259.7	1594.5	85.5	0.336410212	0.100290831
273.9	156.8	217.8	98.2	281.5	62.1	3539.1	1974.1	181.7	1150.8	356.7	91.3	0.051346026	0.092049453
12.3	5.3	13.4	2.7	21.0	62.6	139.7	254.4	19.6	92.5	56.3	22.1	0.139942734	0.076859569
85.9	193.7	77.4	210.8	33.4	212.5	4653.2	1869.2	135.6	2259.5	854.6	79.1	0.029144943	0.072554097
50.6	14.0	63.4	8.6	26.6	29.6	122.9	529.7	32.1	70.8	278.0	21.2	0.261501736	0.060663269